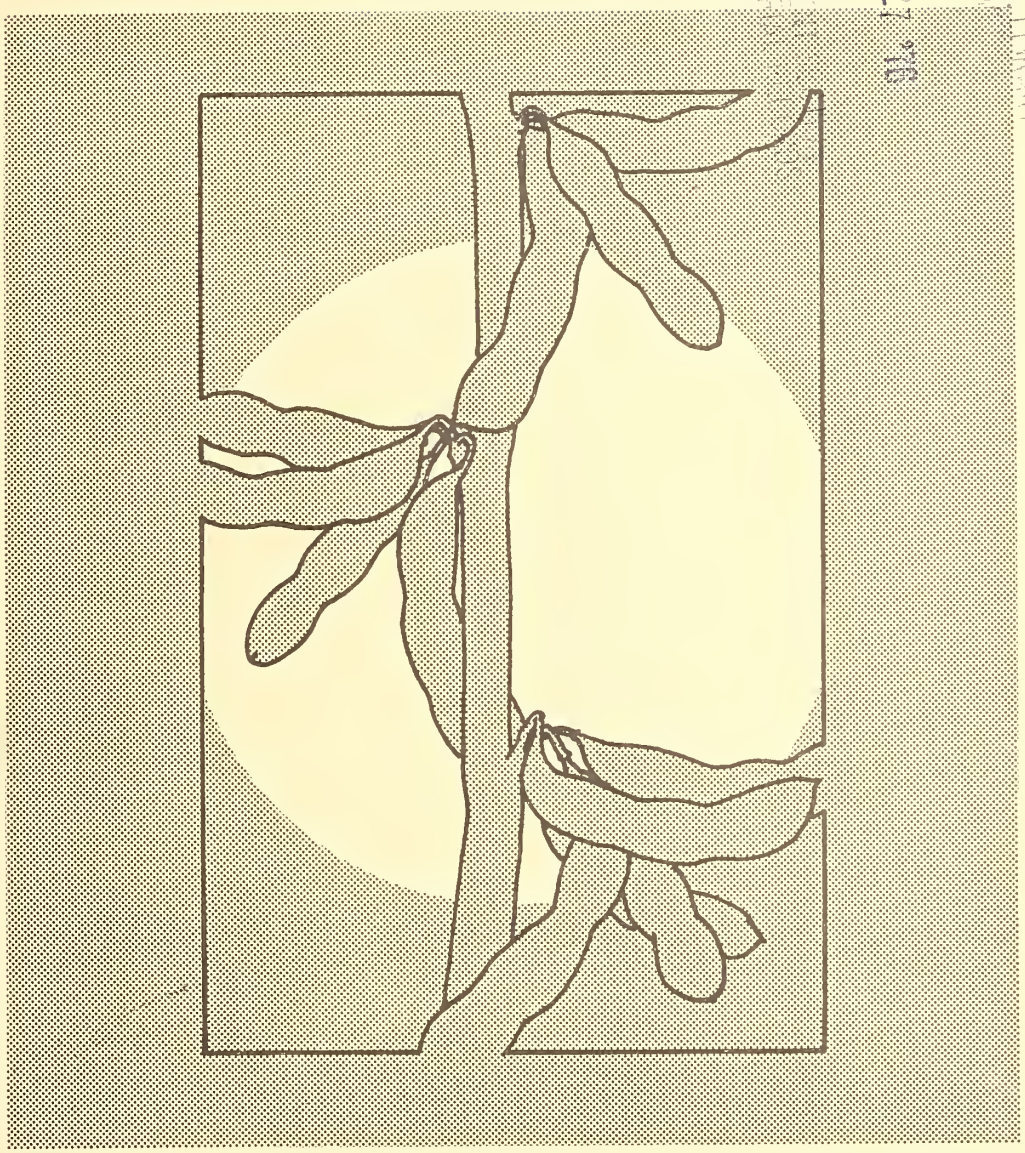
Soybean Genetics Newsletter



Volume 1 **April 1974**

Agricultural Research Service - USDA
and Department of Agronomy
Iowa State University
Ames, Iowa 50010

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I. FOREWORD

Scientists have frequently used newsletters as a means of informal communication. The Maize, Barley, and Pisum Newsletters are familiar examples.

Soybean workers have been a rather small group and were mainly located in Japan and the U.S. Rapid expansion of soybean acreage has been followed by a rapid proliferation in numbers of scientists in many different countries. The need for communication is apparent. In the U.S., we had our first National Soybean Meeting in 1971 and the second was in 1973. An International Soybean Meeting is scheduled for 1975 (see Announcements, this Newsletter).

The Soybean Genetics Newsletter (SGN) will serve as a means of communication at the international level. The Newsletter will have emphasis on genetics and breeding of the soybean and immediate relatives. These areas are broadly interpreted to include research relating to genetics in fields such as biochemistry, entomology, pathology, physiology, taxonomy, etc.

The information in the SGN is of an informal nature to stimulate thought and to exchange ideas. Newsletter articles may be preliminary in nature and speculative in content. Even so, such reports can be exceedingly valuable and helpful, if viewed in the proper perspective.

Publication of this first volume is no small task and we wish to express our sincere thanks to Hollys Heer for her efficient and competent services. The voluntary assistance of Linda Martin, Eke Meister, and Monica Sheridan is gratefully acknowledged.

Acknowledgements

We wish to express our appreciation to the National Soybean Processors Association, whose grant made this issue of the Newsletter possible. We are grateful to Robert W. Judd of the National Soybean Crop Improvement Council for his encouragement and support.

Our thanks go to Rex Heer, student in architecture at Iowa State University, for the cover design.

R. G. Palmer

II. ANNOUNCEMENTS

1. Symposium on Haploids in Higher Plants.

The International Symposium on Haploids in Higher Plants is to be held at the University of Guelph, Guelph, Ontario, Canada, from June 10-14, 1974. The Symposium is endorsed by the International Genetics Federation and organized through an International Program Committee and the University of Guelph. The first four days will consist of invited and contributed papers on the topics of methods of producing haploids and their utilization in plant breeding and research. Workshops will be held on the 5th day. Invited review papers and abstracts of contributed papers will be published in the Proceedings. Abstracts are due March 15, 1974. Those interested in attending or receiving further information should write to:

K. J. Kasha
Crop Science Department
University of Guelph
Guelph, Ontario
Canada N1G 2W1

2. International Conference on Soybeans.

"The International Conference on Soybeans is scheduled to be held at the University of Illinois, Urbana, Illinois during August 3-8, 1975. The program will encompass both production and marketing-utilization aspects of soybean research. We are presently compiling a mailing list and plan to send out formal announcements about April 1. We will ask that people who are interested in receiving additional information advise me so that they will be on a more specific mailing list for the conference."

Dr. R. W. Howell, Head
Department of Agronomy
University of Illinois
Urbana, Illinois 61801
U.S.A.

3. INTSOY, the International Soybean Program.

The International Soybean Program, INTSOY, is a research and education program of the College of Agriculture of the University of Illinois, Urbana-

Champaign, and the University of Puerto Rico, College of Agricultural Sciences, Mayaguez. While it was formally established in 1973, its organizational roots are planted in the long-standing international interests and activities of the University of Illinois in soybeans and of the University of Puerto Rico in food legumes and more recently in soybeans; in the domestic soybean work of the University of Illinois and other cooperating agencies, particularly the U.S. Department of Agriculture; and in the tropical and subtropical expertise and advantages of the University of Puerto Rico.

INTSOY is concerned with all phases of soybeans from planting the seed to consumption, which includes production, harvesting, marketing, processing, and use. The major emphasis is on exploiting the unique potentials of soybeans as a source of protein for direct human consumption. The research thrust centers on the problems of tropical and subtropical environments as potential areas for increasing production, and on nutrition and processing to expand the use of soybean protein foods in human diets.

The INTSOY program is developing cooperative work with and through support of USAID, international research centers, foundations, universities, and other agencies. Outreach activities have been initiated with several countries. Currently, financial support is primarily from the U.S. Agency for International Development. A broadened base of support is anticipated in order to attain the full potential that rests in the International Soybean Program — INTSOY.

INTSOY Newsletter

Regarding our INTSOY Newsletter, we are in process of developing guidelines for its content, frequency of distribution, etc. We hope to have the first issue out within a couple of months and anticipate that it will be issued four to six times each year. The basic purpose of the newsletter is to facilitate communication of those interested in soybean production, marketing, processing, and utilization. It is expected that it will include such information as recent soybean research and extension publications, conferences of interest to soybean workers, soybean activities of individual countries that are of interest beyond country boundaries and International Soybean Program activities — completed, in progress, and planned. We are interested

in obtaining names of individuals or organizations that would like to be put on the mailing list for the INTSOY Newsletter.

For further information regarding INTSOY, please address correspondence to:

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113 Mumford Hall
University of Illinois
Urbana, Illinois 61801
U.S.A.

Telephone: (217) 333-6422

III. REPORT OF SOYBEAN GENETICS COMMITTEE

A. The current members of this committee are:

R. L. Bernard (Chairman)
USRSL
Davenport Hall
Urbana, IL 61801

R. I. Buzzell
Agr. Canada, Res. Station
Harrow, Ontario, NOR IGO,
Canada

R. L. Cooper
USRSL
Davenport Hall
Urbana, IL 61801

H. H. Hadley
Dept. of Agronomy
University of Illinois
Urbana, IL 61801

E. E. Hartwig, USDA
Delta Branch Exp. Station
Soybean Prod. Res.
Stoneville, MS 38776

K. Hinson, USDA
304 Newell Hall
University of Florida
Gainesville, FL 32611

R. G. Palmer, USDA
Agronomy Department
Iowa State University
Ames, IA 50010

B. The duties of this Committee were reviewed and revised at Purdue University April 1, 1974, and the following procedures were established:

1. Maintain Genetic Collection.

The Genetic Collection is divided into four categories:

a. Type Collection includes all published genes of soybeans, preferably in the original strains (excluding U.S. and Canadian name varieties, which are maintained in a separate collection) plus certain mutants or strains that appear to the Committee to have potential genetic interest.

b. Isoline Collection includes adapted varieties Clark, Harosoy and Lee, into which have been backcrossed single genes or combinations of genes.

c. Linkage Collection includes linkage combinations and the various genetic recombinations.

d. Cytological Collection includes translocations, inversions, deficiencies, trisomics, tetraploids, etc.

Collections a, b, and c are maintained at Urbana, Illinois, with R. L. Bernard as curator. Collection d is maintained at Ames, Iowa, with R. G. Palmer as curator.

C. Manuscript review and genetic symbol approval.

The Soybean Genetics Committee requests that researchers submit all manuscripts involving genetic symbols to the Committee Chairman R. L. Bernard. This review by the Genetics Committee will serve to avoid conflict of symbols and will help to insure orderly identification and use of genetic nomenclature. This will also allow assignment of type collection designations (T-numbers) prior to publication, so that these T-numbers may be used in the journal article to identify parental lines.

D. Soybean Genetics Newsletter notes.

All notes for the Newsletter should be sent to R. G. Palmer, who will ask the Soybean Genetics Committee to review those articles that concern genetic symbols. These symbols, reported in the Newsletter, will have the same status as those published in scientific journals.

Rules for Genetic Symbols

I. Gene Symbols

a. A gene symbol shall consist of a base of one to three letters, to which may be appended subscripts and/or superscripts as described below.

b. Genes that are allelic shall be symbolized with the same base letter(s) so that each gene locus will be designated by a characteristic symbol base.

c. The first pair of genes reported for a gene locus shall be differentiated by capitalizing the first letter of the symbol for the dominant or partially dominant allele. (Example: Ab, ab. Ab is allelic and dominant to ab.) If genes are equivalent, codominant,

or if dominance is not consistent, the capitalized symbol may be assigned at the author's discretion.

d. When more than two alleles exist for a locus, the additional alleles or those symbolized subsequently to the pair first published shall be differentiated by adding one or two uncapitalized letters or a number as a superscript to the base. (Example: $\underline{R}$, $\underline{r}^{m}$, $\underline{r}$). This shall be the only use of superscripts. The base for the additional alleles is capitalized only when the gene is dominant or equivalent to the allele originally designated with a capitalized symbol. The superscription may be an abbreviation of a descriptive term. When allelism is discovered for a gene previously assigned a symbol, the previous symbol may be used as the superscript.

e. Gene pairs with the same or similar effects (including duplicate, complementary, or polymeric genes) should be designated with the same letter base differentiated by numerical subscripts, assigning 1, 2, 3, 4, etc., consecutively in the order of publication. (Example: The y-series for chlorophyll deficiency.) This shall be the only use of subscripts. Letter subscripts should not be used. The subscript 1 is automatically a part of the first reported gene symbol for each base but may be omitted until the second symbol is assigned.

f. Base letters may be chosen so as to indicate apparent relationships among traits by using common initial letters for all loci in a related group of traits. Examples are $\underline{P}$ for pubescence type, $\underline{R}$ for disease reaction (plus two initials of the pathogen to complete the base), and $\underline{L}$ for leaf shape.

g. The distinction between traits that are to be symbolized with identical, similar, or with unrelated base letters is necessarily not clear cut. The decision for intermediate cases is at the discretion of the author but should be in accordance with previous practices for the particular type of trait.

The following sections concern supplementary symbols that may be used whenever desired as aids to presentation of genetic formulas.

h. A dash may be used in place of a gene symbol to represent any allele at the indicated locus. The locus represented should be apparent from its position in the formula. (Example: A_ represents both AA and Aa.)

i. A question mark may be used in place of a symbol when the gene is unknown or doubtful, or it may be used as a superscript to the base symbol for the same purpose. (Example: $a^{?}$ indicates that the latter is an unknown allele at the A locus.)

j. Plus symbols may be used in place of the assigned gene symbols of a designated standard homozygous strain when this will facilitate presenting genetic formulas. The standard strain may be any strain selected by the worker, as long as the strain being used and its genetic formula are made explicit.

II. Linkage and Chromosome Symbols

a. Linkage groups and the corresponding chromosomes shall be designated with Arabic numerals. Linkage shall be indicated in a genetic formula by preceding the linked genes with the linkage group number and listing the gene symbols in the order that they occur on the chromosome.

b. Permanent symbols for chromosomal aberrations shall include a symbol denoting the type of aberration plus the chromosome number(s) involved. Specific aberrations involving the same chromosome(s) shall be differentiated by a letter as follows: The symbol Tran shall denote translocations. Tran 1-2a would represent the first case of reciprocal translocations between chromosomes 1 and 2, Tran 1-2b the second, etc. The symbol Def shall denote deficiencies, Inv inversions, and Tris primary trisomics. The first published deficiency in chromosome 1 shall be symbolized as Def 1a, the second as Def 1b, etc. The first published inversion in chromosome 1 shall be denoted as Inv 1a, etc. The first published primary trisomic shall be designated with the Arabic numeral that corresponds to its respective linkage group number.

c. Temporary symbols for chromosomal aberrations are necessary, as it may be many years before they are located on their respective chromosomes. Tran 1 would represent the first case of a published reciprocal translocation; Tran 2, the second case, etc. The first published deficiency shall be symbolized as Def A, the second as Def B, etc. The first published inversion shall be symbolized as Inv A, the second as Inv B, etc. The first published primary trisomic shall be designated as Tris A, the second as Tris B, etc. When appropriate genetic and/or cytological evidence is available, the temporary symbols should be replaced with permanent symbols, with the approval of the Soybean Genetics Committee.

III. Cytoplasmic Factor Symbols

a. Cytoplasmic factors shall be designated with one or more letters prefixed by cyt-. (Example: cyt-G indicates the cytoplasmic factor for maternal green cotyledons, cyt-Y indicates that for maternal yellow cotyledons.)

IV. Priority and Validity of Symbols

a. A symbol shall be considered valid only when published in a recognized scientific journal, or when reported in the Soybean Genetics Newsletter, with conclusions adequately supported by data which establish the existence of the entity being symbolized. Publication should include an adequate description of the phenotype in biological terminology, including quantitative measurements wherever pertinent.

b. In cases where different symbols have been assigned to the same factor, the symbol which was first published should be the accepted symbol, unless the original interpretation is shown to be incorrect, the symbol is not in accordance with these rules, or additional evidence shows that such a change is necessary.

V. Rule Changes

These rules may be revised or amended by a majority vote of the Soybean Genetics Committee.

IV. RESEARCH NOTES

AGRICULTURE CANADA
Research Station
Harrow, Ontario

1. Soybean genetic studies at Harrow.

Nine flavonol glycosides occur in various soybean cultivars with gene $\underline{t}_1$ resulting in kaempferol and $\underline{T}_1$ controlling the presence of quercetin plus kaempferol (Buttery and Buzzell, 1973). The sugars of these glycosides have been identified and four flavonol glycoside genes have been studied (Buzzell and Buttery, 1973, and unpublished). A monoglucoside is the basic glycoside; it is present even when the four genes are recessive. The dominant alleles of the four genes control (probably through appropriate glycosyl transferases) the addition of glucose or rhamnose units to the glucose of the monoglucoside in the formation of four diglycosides and four branched triglycosides. Gene $\underline{Fg}_1$ adds a glucose by a β (1-6) linkage (i.e. position 6 of the "mono" glucose) to form the gentiobioside; $\underline{Fg}_2$ adds rhamnose α (1-6) to form the rutinoside; $\underline{Fg}_3$ adds glucose β (1-2) to form the sophoroside; and $\underline{Fg}_4$ adds rhamnose α (1-2) to form the neohesperidoside. In gene combinations, $\underline{Fg}_1$ plus $\underline{Fg}_3$, $\underline{Fg}_1$ plus $\underline{Fg}_4$, $\underline{Fg}_2$ plus $\underline{Fg}_3$, and $\underline{Fg}_2$ plus $\underline{Fg}_4$ form the 2^G-glucosyl gentiobioside, the 2^G-rhamnosyl gentiobioside, the 2^G-glucosyl rutinoside and the 2^G-rhamnosyl rutinoside, respectively. In the other two gene combinations, $\underline{Fg}_1$ and $\underline{Fg}_2$ both involve a 1-6 linkage while $\underline{Fg}_3$ and $\underline{Fg}_4$ both involve a 1-2 linkage; thus no triglycosides are formed because the same position of the "mono" glucose is involved in each case.

The genes Eu and eu control fast-running and slow-running isoenzymes of urease in soybean seeds (Buttery and Buzzell, 1971); both urease types have high activity. In a survey of 400 varieties and plant introductions, no other types were found. However, in Glycine soja, two accessions, PI 326.581 and PI 326.582, had slow-running urease with low activity. Genetic study to date indicates that another gene may be involved.

Powdery mildew studies have shown that resistance to Microsphaera diffusa is controlled by a single dominant gene, and that resistance to

Erysiphe pisi (polygoni) is controlled by a single recessive gene. These genes are probably non-allelic.

Using the Arkansas male sterility (Caviness, Walters, and Johnson, 1970), the F_2 of S571-26 x Columbia was tested; 137 fertile : 43 male sterile plants were obtained, indicating that a recessive gene is involved. Sterility was visually classified (using magnifying glasses) as having shrivelled, discolored anthers with a lack of abundant pollen. The appearance of the anthers is different from those affected by $\underline{ms}_1$. Male sterile segregations are being tested in other material.

Using the day-neutrality characterized by Polson (1972), the F_2 of OX301 x PI 297.550 was tested in a growth cabinet at 25 C using a 20 hour daylength. A mixture of incandescent and fluorescent light was used with the light intensity remaining the same over the 20 hrs. At 35 days after planting, 34 plants were non-flowering the same as OX301, and 14 plants were flowering or had well-developed buds the same as the PI. Three F_3 plants of each of the 14 flowering plants were tested under the same conditions; they all flowered in 35 days. Possibly a recessive gene is involved that decreases sensitivity to "long" daylength. The PI and OX301 both give an insensitive fluorescent-daylength response (Buzzell, 1971) and should carry $\underline{e}_3$. If the soybean originated as a short-day tropical plant, its evolutionary adaptation to higher latitudes could have come about through the accumulation of recessive mutations for genes that control the short-day response. The recessive genes $\underline{e}_1$ and $\underline{e}_2$ both result in earlier flowering and maturity (Bernard, 1971).

Seed-coat compounds are being studied. Of the flavonol glycoside genes, $\underline{Fg}_2$ has an apparent effect upon compounds that occur in black and brown ($\underline{T}_1$) seed coats. The cyanidin-3-monoglucoside occurs in all black seed coats but when $\underline{W}_1$ is present an additional glycoside is formed. Gene $\underline{t}_2$, which reduces the quercetin ($\underline{T}_1$) content of the pubescence without an effect upon quercetin glycoside formation in the leaves, has no apparent effect upon seed-coat compounds. The wm gene, which reduces flavonol content of leaves and flowers, is being tested for possible effects upon seed-coat compounds.

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Bernard, R. L. 1971. Two major genes for time of flowering and maturity in soybeans. Crop Sci. 11:242-244.

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Buzzell, R. I. and B. R. Buttery. 1973. Inheritance of flavonol glycosides in soybeans. Can. J. Genet. Cytol. 15:865-867.

Caviness, C. E., H. J. Walters and D. L. Johnson. 1970. A partially male sterile strain of soybean. Crop Sci. 10:107-108.

Polson, D. E. 1972. Day-neutrality in soybeans. Crop Sci. 12:773-776.

R. I. Buzzell
B. R. Buttery
J. H. Haas

2. Soybean linkage tests.

I am especially intrigued by the occurrence in soybeans of "duplicate" genes, that is, genes with a similar or related function. Additional genetic studies and mapping of the chromosomes might give us a clue as to the evolution of the soybean. Such information could provide a better understanding of gene action in this species, and thereby would be helpful to breeding programs. Thus, biochemical and physiological means are being used at Harrow to characterize additional genes, with attention being given to tests for allelism and linkage.

F_2 linkage results are presented in Table 1 with a = XY, b = Xy, c = xY, and d = xy for the gene pairs listed in the form of Xx and Yy. Percentage recombination was obtained from the ratio of products following Immer and Henderson (1943). In the case of $\underline{E}_3\underline{e}_3$, the F_2 was classified on the basis of F_3 progeny tests.

Gene $\underline{Fg}_4\underline{fg}_4$ is linked with $\underline{T}_1\underline{t}_1$ (Linkage Group I) and $\underline{Fg}_3\underline{fg}_3$ and $\underline{Fg}_4$ $\underline{fg}_4$ are linked. The $\underline{Fg}_4\underline{T}_1$, $\underline{Fg}_4\underline{t}_1$, and $\underline{fg}_4\underline{T}_1$ types are available but the $\underline{fg}_4\underline{t}_1$ crossover type has not been obtained, nor observed in cultivars. Another cross will be used that will be more suitable for detecting $\underline{fg}_4\underline{t}_1$,

and three-point tests will be made for Linkage Group I. Genes $\underline{Fg_1}$ and $\underline{Fg_2}$ did not show linkage with $\underline{Rr}$ (II), $\underline{P_2p_2}$ (IV), and $\underline{Ii}$ (VII). None of the other gene pairs show close linkage; most likely they are independent but further evidence is needed in some cases.

Table 1

Soybean F_2 linkage tests

Genes		a	b	c	d	Sum	%R	SE	Phase
		Columbia ($\underline{Fg_1}fg_2\underline{fg_3}$) x Mukden ($\underline{fg_1}\underline{Fg_2}\underline{Fg_3}$)							
Fg_1fg_1	Fg_2fg_2	202	66	56	25	349	54	3.8	R
Fg_1fg_1	Fg_3fg_3	205	63	61	20	349	51	4.0	R
Fg_2fg_2	Fg_3fg_3	197	61	69	22	349	50	4.0	C
		Blackhawk ($\underline{fg_1}\underline{fg_2}\underline{Fg_3}\underline{e_3}\underline{w_1}\underline{ep}$) x Medium Green ($\underline{Fg_1}\underline{Fg_2}\underline{fg_3}\underline{E_3}\underline{W_1}\underline{Ep}$)							
Fg_1fg_1	Fg_2fg_2	92	32	23	9	156	48	5.9	C
Fg_1fg_1	Fg_3fg_3	99	22	25	10	156	I		R
Fg_2fg_2	Fg_3fg_3	85	30	36	5	156	37	6.8	R
Fg_1fg_1	E_3e_3	90	34	25	6	155	I		C
Fg_1fg_1	W_1w_1	93	30	21	12	156	42	5.4	C
Fg_1fg_1	Epep	96	28	28	4	156	I		C
Fg_2fg_2	E_3e_3	84	31	31	9	155	53	6.2	C
Fg_2fg_2	W_1w_1	84	31	30	11	156	50	6.0	C
Fg_2fg_2	Epep	95	20	29	12	156	40	5.3	C
Fg_3fg_3	E_3e_3	90	30	25	10	155	53	5.8	R
Fg_3fg_3	W_1w_1	94	26	20	16	156	I		R
Fg_3fg_3	Epep	91	27	33	5	156	41	6.6	R
E_3e_3	W_1w_1	84	29	31	11	155	50	6.0	C
E_3e_3	Epep	95	20	28	12	155	40	5.4	C
W_1w_1	Epep	94	20	30	12	156	41	5.4	C
		AK-FC30.761 ($\underline{Fg_2}\underline{fg_4}\underline{T_1}$) x Beeson ($\underline{fg_2}\underline{Fg_4}\underline{t_1}$)							
Fg_2fg_2	Fg_4fg_4	121	48	37	15	221	I		R
Fg_2fg_2	T_1t_1	131	38	43	9	221	I		C
Fg_4fg_4	T_1t_1	111	47	63	0	221	0	0.0	R

Table 1 (continued)

Genes		a	b	c	d	Sum	%R	SE	Phase
T31 ($\underline{Fg_1}\underline{Fg_2}\underline{Fg_3}\underline{Fg_4}\underline{rp_2}\underline{iW_1}$) x OX936 ($\underline{fg_1}\underline{fg_2}\underline{fg_3}\underline{fg_4}\underline{RP_2}\underline{Iw_1}$)									
Fg_1fg_1	Fg_2fg_2	202	69	63	23	357	49	3.9	C
Fg_1fg_1	Fg_3fg_3	199	72	67	19	357	53	4.0	C
Fg_1fg_1	Fg_4fg_4	200	71	69	17	357	I		C
Fg_2fg_2	Fg_3fg_3	201	64	65	27	357	46	3.8	C
Fg_2fg_2	Fg_4fg_4	206	59	63	29	357	44	3.7	C
Fg_3fg_3	Fg_4fg_4	247	19	20	71	357	12	1.8	C
Fg_1fg_1	Rr	130	39	39	14	222	52	4.9	R
Fg_2fg_2	Rr	125	44	42	11	222	46	5.2	R
Fg_3fg_3	Rr	126	41	43	12	222	48	5.1	R
Fg_4fg_4	Rr	129	40	40	13	222	50	5.0	R
Fg_1fg_1	P_2p_2	208	63	62	24	357	53	3.8	R
Fg_2fg_2	P_2p_2	201	65	69	22	357	50	4.0	R
Fg_3fg_3	P_2p_2	205	62	65	25	357	53	3.8	R
Fg_4fg_4	P_2p_2	208	61	62	26	357	55	3.7	R
Fg_1fg_1	Ii	188	74	58	25	345	51	4.0	R
Fg_2fg_2	Ii	182	75	64	24	345	49	4.1	R
Fg_3fg_3	Ii	187	71	59	28	345	53	3.9	R
Fg_4fg_4	Ii	188	73	58	26	345	52	3.9	R
Fg_1fg_1	W_1w_1	210	59	66	21	355	48	3.9	C
Fg_2fg_2	W_1w_1	204	61	72	18	355	52	4.1	C
Fg_3fg_3	W_1w_1	200	65	76	14	355	I		C
Fg_4fg_4	W_1w_1	206	62	70	17	355	53	4.1	C
W_1w_1	Rr	133	38	37	15	223	55	4.7	R
W_1w_1	P_2p_2	213	58	62	23	356	54	3.8	R
W_1w_1	Ii	199	72	46	28	345	I		R
"New white" ($\underline{w_4}\underline{WmT_1}$) x T235 ($\underline{W_4}\underline{wmt_1}$)									
W_4w_4	Wmwm	71	22	25	8	126	50	6.7	R
W_4w_4	T_1t_1	72	21	23	10	126	I		R
Wmwm	T_1t_1	75	21	20	10	126	42	6.1	C

References

Immer, F. R. and M. T. Henderson. 1943. Linkage studies in barley. Genetics 28:419-440.

R. I. Buzzell

AGRICULTURE CANADA
Research Station
Harrow, Ontario

and

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U.S. Regional Soybean Laboratory
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1. Inheritance of magenta flower color.

In an increase plot of foundation seeds of Harosoy in 1957 at Urbana, a number of Harosoy-type plants were found with flowers of a deeper red than the normal purple (P). The color is best described as magenta (M). This mutant was added to the Genetic Type Collection as T235. Results were obtained at Urbana which indicated that a single recessive gene, wm, was involved. It was not allelic to W_1. The F_1 of T235 (M) x Harosoy (P) was purple and the F_2 segregated 128P : 56M; F_3 progeny tests showed that 12 purple F_2 plants produced only P, 44 purple segregated P and M (1174 : 384 in total), and 29 magenta gave only M. The F_1 of C1128 (white, W) x T235 (M) was purple and the F_2 segregated 154P : 64M : 93W.

In conjunction with a leaf-flavonoid study (Buttery and Buzzell, 1973) at Harrow we observed that, in comparison to Harosoy, the amount of the leaf-flavonol glycosides K1, K2, and K5 was greatly reduced in T235. Fuming the flowers of T235 with ammonia indicated that there was a reduction in flavonol content, i.e. they had blue standards and cream-colored wings in contrast to green standards and yellowish wings for purple flowers, and bright yellow standards and wings for white flowers. From the cross of E. E. Hartwig's "New white" strain x T235, white-flowered plants with reduced leaf flavonol content were obtained that upon fuming gave only a slight change from white to a dull cream color. The wm gene was not allelic to W_4.

By using leaf-flavonol tests and fuming tests of flowers, the F_2 of W x M crosses should be separable into four classes as follows:

Genotypes	Expected ratio	Flower color	Flavonol content of leaves & flowers
$\underline{W}_1$ - $\underline{Wm}$ -	9	Purple	Normal (N)
$\underline{W}_1$ - $\underline{wmwm}$	3	Magenta	Reduced (R)
$\underline{w}_1\underline{w}_1$ $\underline{Wm}$ -	3	White	Normal (N)
$\underline{w}_1\underline{w}_1$ $\underline{wmwm}$	1	White	Reduced (R)

The white-flowered L62-904 (backcross strain of Harosoy) was crossed with T235; i.e., $\underline{w}_1\underline{w}_1\underline{Wm}\underline{Wm}$ x $\underline{W}_1\underline{W}_1\underline{wm}\underline{wm}$. The F_2 segregated 47P : 24M : 25 W-N : 0 W-R whereas 54 : 18 : 18 : 6 were expected for a 9 : 3 : 3 : 1 ratio with independent segregation. In the F_3 of the purple F_2 plants, 40 segregated P, M, and W (N or R?), 3 segregated P and M, and 4 segregated P and W (N or R). All progenies of magenta plants were magenta. Fuming tests of the F_3 of the 25 white-flowered F_2 plants revealed that 5 were segregating W-N : W-R (in total 66 : 23 plants). These results were confirmed by leaf-flavonol tests. Thus, $\underline{wm}$ is linked with $\underline{W}_1$ (recombination estimated to be 11%). Since there is no known linkage involving $\underline{W}_1$, this could be a new linkage group. Additional tests are being run with larger populations.

The fact that the magenta characteristic does not occur in commercial and introduced varieties indicates that it might be a deleterious mutant. Magenta-flowered plants often develop a distinctive reddish-purple discoloration of the leaves as the plants approach maturity. In the U.S. Regional Soybean Tests, magenta isolines averaged 3% less in yield than the corresponding purple-flowered Harosoy. In a field test at Harrow, T235 had a lower photosynthetic rate and lower specific leaf weight than Harosoy. The $\underline{w}_1\underline{w}_1$ $\underline{wmwm}$ genotype will be tested to determine whether the observed effects are caused by a decrease in flavonols or an increase in cyanidins.

References

Buttery, B. R. and R. I. Buzzell, 1973. Varietal differences in leaf flavonoids of soybeans. Crop Sci. 13:103-106.

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1. An induced crinkled leaf mutant in soybean.

One M_3 progeny row of irradiated 'Lee' soybean (20 kr gamma rays) showed segregation for leaf crinkling. From a total of 12 plants in this progeny row, two showed severe crinkling and puckering of leaves. It looked as if these plants were suffering from viral disease. The other 10 plants looked normal initially, but in later stages showed minor crinkling of leaves.

In order to test whether it was due to genetic factors, physiological disorder, or viral infection, the seeds from all the individual plants were harvested and kept separately. The individual progeny rows were planted in 1972. All the progenies of two plants which showed severe crinkling in the previous year showed severe crinkling again. The other 10 progenies segregated for plants with normal and 'crinkled leaf', as given in Table 1. The ratio of plants with normal and 'crinkled leaves' fitted very closely to a 3 : 1 ratio with no heterogeneity among the families. Later in the season some of the normal plants showed minor crinkling but no attempt was made to classify them. On the basis of the observations made in the previous year, the heterozygotes develop minor crinkling in later stages. Thus, the inheritance of this trait appears to be governed by a single recessive gene pair.

The plants with crinkled leaf looked normal in all other respects. These plants were almost of the same height, with slightly fewer pods. Therefore, this character is different than the 'pseudo-mosaic' reported by Probst (1950).

References

Probst, A. H. 1950. The inheritance of leaf abscission and other characters in soybean. Agron. J. 42:35-45.

Table 1
Segregation for plants with normal and crinkled leaves in M_4 progeny rows

Progeny number	Number of plants with: Normal leaf	Number of plants with: Crinkled leaf	χ^2 (3 : 1)
1	82	24	0.310
2	72	23	0.032
3	57	18	0.040
4	60	20	0.000
5	69	26	0.280
6	32	8	0.533
7	35	11	0.029
8	94	32	0.010
9	92	33	0.134
10	34	12	0.029
Pooled	627	207	0.014
Heterogeneity (9df)			1.476

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2. PI 171.443 and G. formosana — resistant lines for yellow mosaic of soybean.

Yellow mosaic is one of the most serious diseases of soybean in northern plains of India. It has also been observed in certain parts of south India. It is caused by a virus which is transmitted through a white fly (Bemisia tabaci) (Nene, 1969). The leaves develop yellow patches. With the severity of the disease, the yellow patches increase in size and cover the whole leaf. Depending upon the stage at which infection occurs, the yield losses may be quite substantial. There is no report about resistant sources for this disease in soybean. Therefore, a systematic screening of soybean

germplasm was initiated in 1970 in order to identify resistant lines for this disease. Since then, about 5000 lines including about 3200 lines from USDA (obtained in 1971 through the courtesy of E. E. Hartwig and R. L. Bernard) have been screened. Out of all these lines, only two, PI 171.443 and G. formosana [probably a variant of G. ussuriensis (G. soja) obtained through the courtesy of K. L. Chan, Taiwan Agricultural Research Institute, Taipei] were found to be resistant. The resistance of these lines was first noticed in 1971. These lines were further screened in 1972 and 1973 in multi-row plots and at several dates of planting, along with susceptible checks such as 'Bragg', 'Lee' and others. In all these plantings, PI 171.443 and G. formosana remained completely free from yellow mosaic, whereas all other varieties were severely affected.

PI 171.443 is originally an introduction from China. It has erect, indeterminate plant type with white flowers and tawny pubescence. It belongs to maturity group VI. The seeds are of chocolate color with black concentric marks on them. This line is otherwise highly susceptible to pod blight, bacterial pustule and rust (Phakopsora pachyrhizi).

G. formosana is a typical wild-looking soybean with small very narrow leaves and prostrate growth habit. It flowers in about 85 days and matures in about 130 days. It has tawny pubescence and purple flowers. It is susceptible to bacterial pustule and rust. It can be easily crossed with cultivated varieties of soybean.

A number of segregating populations have been generated using these lines as source of resistance for yellow mosaic. The inheritance, as well as the nature of resistance to yellow mosaic, is being investigated.

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3. Induced male-sterile mutants in soybeans.

The importance of inducing mutations through irradiation has been well established in many crops. However, only limited use of this technique has been made in soybean. A mutation breeding program in soybeans was initiated in 1970 at this station to create useful mutations, particularly for male-sterility, since no male-sterile-female-fertile line had been reported by then.

Varieties 'Clark 63', 'Lee', 'Bragg' and 'Semmes' were irradiated with 8, 12, 16 and 20 kr of gamma rays in spring 1970. The M_1 generation was grown in spring 1970. M_2 and M_3 generations were evaluated in the rainy seasons of 1970 and 1971 respectively. Two M_3 progenies of irradiated Semmes (20 kr) showed segregation for sterile plants which looked completely green at maturity and had only a few pods. These were designated as 'Semmes M.S.1' and 'Semmes M.S.2'. Semmes M.S.1 had 38 normal and 11 sterile plants and Semmes M.S.2 had 42 normal and 12 sterile plants, both of which fitted very closely to 3:1 ratio. The sterile plants of Semmes M.S.2 had relatively more pods than those of Semmes M.S.1. Seeds from all the normal and sterile plants from both progenies were harvested separately. Twenty-four normal plant progenies and all the seeds from sterile plants from each line were planted in the rainy season of 1972. Thirty normal plant progenies derived from 'N 69-2774', a male-sterile maintainer line supplied by C. A. Brim in 1971, were also planted for comparative study. At the time of flowering, male-sterile plants were identified by examining the pollen, and further pollen studies were made. The classification between normal and sterile plants was made at the time of maturity. The results are summarized below.

Semmes M.S.1: From the 24 progenies planted, only 17 germinated. Of these, 10 segregated for male sterility and 7 bred true for normal plants, which fitted to a 2:1 ratio. The ratio of normal and sterile plants in each of the 10 segregating families, as well as the pooled values, indicated a close fit to a 3:1 ratio with no heterogeneity among the families. On an average, only about 30% pollen grains from the male-sterile plants took aceto-carmine stain, and there was some variation in the size ranging from 0.027mm to 0.0325mm. The number of pods on sterile plants ranged from 0 to 5, indicating some female fertility.

Semmes M.S.2: From 24 normal plant progenies planted, only 23 germinated, of which 19 segregated for male sterility and 5 bred true for normal plants, which fitted to a 2:1 ratio. The ratio of normal and sterile plants in each of the 19 segregating progenies, as well as the pooled values, fitted very closely to a 3:1 ratio with no heterogeneity among the families. There was very little or no pollen in the anthers (of any stage) obtained from the sterile plants of this line. The number of pods on these sterile plants ranged from 5 to 85 (mostly between 20 to 60) indicating more female fertility. The seeds obtained from the sterile plants in previous year gave mostly normal plants and a few sterile plants.

N 69-2774: Of 30 normal plant progenies, 22 segregated for sterility and 8 bred true for normal plants which fitted to a 2:1 ratio. The ratio of normal to sterile plants in each of the 22 segregating progenies, as well as the pooled values, indicated a close fit to a 3:1 ratio, with no heterogeneity among the families. This was in conformity with the results of Brim and Young (1971), indicating the monogenic inheritance of sterility in this line.

About 35% pollen grains from the male sterile plants took acetocarmine stain and others looked empty. However, there was considerable variation from plant to plant. There was a striking difference in the pollen size of sterile and normal plants in this line. The pollen size of sterile plants ranged from 0.04mm to 0.06mm as compared to 0.0275 to 0.0325mm of normal plants. The number of pods on the male sterile plants in this line ranged from 1 to 50 (mostly between 10 to 30).

Thus, the inheritance studies indicate that sterility in all the three lines is governed by single gene pairs. However, the pollen studies and the differential pod set on the male sterile plants indicate that the genes for sterility are different in different lines. Further genetic studies, including chromosomal basis and pollen behavior, are in progress, on completion of which gene symbols will be assigned.

References

Brim, C. A. and M. F. Young. 1971. Inheritance of a male sterile character in soybeans. Crop Sci. 11: 564-566.

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1. Genetics of the meiotic mutant $\underline{st_4}$.*

In 1968 Walter R. Fehr, Department of Agronomy, Iowa State University, observed sterile plants in a single plant progeny row of the cultivar 'Hark'. Further analyses by Fehr indicated that sterility existed in both sexes and that it was a recessive genetic trait (Fehr, personal communication, 1970).

The current research effort began in 1970. Fertile plants from segregating progenies were threshed individually in 1970, 1971, 1972 and 1973. These progenies were evaluated each succeeding year and data were recorded for number of segregating progenies (Table 1), ratio of fertile plants : sterile plants (Table 2), and seed set on the near-sterile plants (Table 3). The data in Tables 1 and 2 support the hypothesis that sterility is associated with the homozygous condition of a single recessive gene.

We were interested in the number of seeds produced on the near-sterile plants and in their chromosome constitution. There was considerable variation in seed set from year to year (Table 3). This was particularly evident in the number of seeds per near-sterile plant within line T258** : 1 seed per 7.4 sterile plants in 1971; 1 seed per 22.2 sterile plants in 1972; 1 seed per 18.7 sterile plants in 1973. These differences are also reflected in the percent completely sterile plants for the three different years (Table 3). There was no noticeable difference in the number of flowers per plant in the three years.

Interestingly, two different F_2 populations grown in 1973 in which the $\underline{st_4}$** gene was segregating had fewer completely sterile plants than the original line (Table 3). Similarly, we observed 1 seed per 3.5 sterile plants and 1 seed per 4.5 sterile plants, respectively, for the two different

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**Genetic type collection T-number and gene symbol assigned by Soybean Genetics Committee, January, 1974.

F_2 populations. The most likely explanation for the differences observed between the original line and the F_2 populations is genotype x environment interaction.

Pollen from fertile and sterile plants of T258 was classified for stainability using I_2KI. The percentage of plump and well-stained pollen grains from fertile and sterile plants was 97.3 and 2.7, respectively. Pollen grains from sterile plants varied greatly in size. Some grains were collapsed, devoid of starch and smaller than grains from fertile sibs; some were considerably larger.

Cytological observations were made of meiotic chromosomes in sterile plants. The earlier meiotic stages in soybeans are not amenable to detailed cytological study and presently we cannot distinguish between desynapsis and asynapsis of the chromosomes.

Two asynaptic mutants in soybeans, T241 and T242, were described by Hadley and Starnes (1964). Allelism tests were conducted with T241 and T258 (Table 4); and with T242 and T258 (Table 5). In Table 4, progenies in five F_2 families (PR 19-2, 25-2, 28-2, 29-1, and 29-4) represent a 3:1 population. The remaining five families represent a 9:7 population. If segregation for sterility were at two loci and if the steriles were phenotypically similar, the expected ratio would be 9 fertile : 7 sterile. Similarly in Table 5, the F_2 families fit into two discrete populations, one representing a 3:1 segregation, the other a 9:7 segregation. Therefore, from the data presented in Tables 4 and 5, we can conclude that $\underline{st}_4$ is a different locus than $\underline{st}_2$ and $\underline{st}_3$.

T241 has white flowers (w) and tawny pubescence (T); T242 has purple flowers (W) and gray pubescence (t); and T258 has purple flowers and gray pubescence. Chi-square tests for independent assortment between $\underline{st}_4$ and flower color, $\underline{st}_4$ and pubescence color were calculated. The data gave no indication of linkage.

We are determining mitotic chromosome numbers of progeny produced by the homozygous $\underline{st}_4$ plants. The diploid chromosome number of soybeans is 2N=40. Aneuploids between 40-45 chromosomes have been identified. Aneuploids are also found at the tetraploid level.

Table 1

Segregating and nonsegregating F_2 families in T258 for 1971, 1972, 1973 (expected ratio — 2 segregating : 1 nonsegregating)

Year	Segregating	Nonsegregating	χ^2	Probability
1971	95	42	0.4416	.75-.50
1972*	39	28	2.1567	.25-.10
1973	28	15	0.0465	.90-.75
Total	162	85	2.6448	
Pooled chi-square (1df)			0.1296	.75-.50
Homogeneity chi-square (2df)			2.5152	.50-.25

*One family had segregating ratios of 1 segregating : 7 nonsegregating progenies rather than the expected 2:1 ratio and is not included.

Table 2

Fertile and sterile plants in segregating F_2 families of T258 and T258 crosses (expected ratio — 3 fertile : 1 sterile)

Year	Fertile	Sterile	χ^2	Probability
1971*	1099	353	0.3673	.75-.50
1972	1106	400	1.9557	.25-.10
1973	809	281	0.3535	.75-.50
1973**	390	128	0.0232	.90-.75
1973***	926	322	0.4274	.75-.50
Total	4330	1484	3.1271	
Pooled chi-square (1df)			0.85	.50-.25
Homogeneity chi-square (4df)			2.2771	.75-.50

*Includes only 66 of the 95 segregating families.

**Segregating F_2 families from crosses between homozygous fertile plants of T241 and heterozygous fertile plants of T258.

***Segregating F_2 families from crosses between homozygous fertile plants of T242 and heterozygous fertile plants of T258.

Table 3

Number of seeds from $\underline{st_4st_4}$ plants

Number of seeds per plant	Number of plants				
	1971*	1972*	1973*	1973**	1973***
0	519	385	267	100	261
1	58	13	13	23	55
2	11	1	1	2	4
3	0	1	0	2	1
4	0	0	0	1	0
5					0
6					1
Total number of plants	588	400	281	128	322
Total number of seeds	80	18	15	37	72
% plants with no seeds	88	96	95	78	81

*Segregating F_2 families of T258.

**Segregating F_2 families from crosses between homozygous fertile plants of T241 and heterozygous fertile plants of T258.

***Segregating F_2 families from crosses between homozygous fertile plants of T242 and heterozygous fertile plants of T258.

Table 4

Observed ratios in segregating F_2 families from crosses between heterozygous fertile plants of T241 and heterozygous fertile plants of T258

Families that were considered to be samples from a 3:1 population of $\underline{St}_2\ \underline{St}_2\ \underline{St}_4\ \underline{st}_4$ or $\underline{St}_2\ \underline{st}_2\ \underline{St}_4\ \underline{St}_4$ F_2 plants

F_2 number	Fertile	Sterile	Chi-square and probability for expected ratios			
			χ^2(3:1)	P	χ^2(9:7)	P
PR 19-2	69	23	0.0	0	13.14	<.005
PR 25-2	112	42	0.42	.75-.50	16.99	<.005
PR 28-2	122	44	0.20	.75-.50	20.06	<.005
PR 29-1	88	35	0.78	.50-.25	11.69	<.005
PR 29-4	186	74	1.66	.25-.10	24.69	<.005

Families that were considered to be samples from a 9:7 population of $\underline{St}_2\ \underline{st}_2\ \underline{St}_4\ \underline{st}_4$ F_2 plants

F_2 number	Fertile	Sterile	Chi-square and probability for expected ratios			
			χ^2(3:1)	P	χ^2(9:7)	P
PR 19-1	106	82	34.75	<.005	0.001	.975-.95
PR 25-1	67	57	29.08	<.005	0.25	.75-.50
PR 26-1	61	47	19.75	<.005	0.002	.975-.95
PR 28-1	46	42	24.24	<.005	0.57	.50-.25
PR 29-5	57	39	12.50	<.005	0.38	.75-.50

Table 5

Observed ratios in segregating F_2 families from crosses between heterozygous fertile plants of T242 and heterozygous fertile plants of T258

Families that were considered to be samples from a 3:1 population of $\underline{St}_3\ \underline{St}_3\ \underline{St}_4\ \underline{st}_4$ or $\underline{St}_3\ \underline{st}_3\ \underline{St}_4\ \underline{St}_4$ F_2 plants

F_2 number	Fertile	Sterile	Chi-square and probability for expected ratios			
			χ^2(3:1)	P	χ^2(9:7)	P
PR 2-1	71	21	0.23	.75-.50	16.37	<.005
PR 15-2	146	58	1.28	.50-.25	19.45	<.005
PR 15-3	127	42	0.002	.975-.95	24.53	<.005
A 1258-1	190	76	1.81	.25-.10	24.90	<.005
A 1258-2	294	108	0.75	.50-.25	46.57	<.005
A 1260-1	238	77	0.05	.90-.75	47.71	<.005
A 1260-2	268	94	0.18	.75-.50	46.52	<.005

Families that were considered to be samples from a 9:7 population of $\underline{St}_3\ \underline{st}_3\ \underline{St}_4\ \underline{st}_4$ F_2 plants

F_2 number	Fertile	Sterile	Chi-square and probability for expected ratios			
			χ^2(3:1)	P	χ^2(9:7)	P
PR 10-1	47	31	9.04	<.005	0.51	.50-.25
PR 13-1	42	26	6.35	.025-.01	0.84	.50-.25
PR 13-2	87	63	23.12	<.005	0.19	.75-.50
PR 13-3	50	30	6.67	.01-.005	1.27	.50-.25
PR 13-4	27	20	7.72	.01-.005	0.03	.90-.75
PR 13-5	32	18	3.23	.01-.005	1.22	.50-.25
A 1258-3	229	180	78.83	<.005	0.01	.95-.90
A 1261-1	222	153	49.93	<.005	1.33	.25-.10
A 1261-2	156	143	83.09	<.005	2.02	.25-.10

References

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2. Male transmission of an extra chromosome.*

Three primary trisomes were studied in 1973. Two trisomes originated from an asynaptic T241 ($\underline{st}_2\ \underline{st}_2$) plant; the other trisome came from a T258 ($\underline{st}_4\ \underline{st}_4$) plant. We had previously observed 42-chromosome plants among the selfed progeny of 41-chromosome plants and we suspected simultaneous female and male transmission of the extra chromosome. We were also interested in testing to determine if the extra chromosomes present in the three trisomes were identical or different. Therefore, the trisomes were reciprocally intercrossed, crossed both as male and female parents with the cultivar 'Hark' and also selfed. Chromosome numbers of the parental trisomes and F_1 plants were determined from root tip squash preparations.

Observations on male transmission of the extra chromosome are presented in Table 1. The values for male transmission of each trisome, A73-T23**, A73-T25**, and A73-T33***, are very high (approximately 25%), when compared with published reports describing primary trisomes in other plant species (generally 0 to 15%). Additional F_1 seedlings will be classified for chromosome number to determine if the values obtained are representative of male transmission in soybeans. The identity of the three trisomes will be established in the summer of 1974.

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*Research supported in part by a grant from the American Soybean Association Research Foundation.

**From a T241 ($\underline{st}_2\ \underline{st}_2$) plant.

***From a T258 ($\underline{st}_4\ \underline{st}_4$) plant.

Table 1

Male transmission of an extra chromosome in three primary trisomes in soybeans

Female parent (40 chromosomes) Cultivar		Male parent (41 chromosomes) Plant No.	Frequency of F_1 seedlings with 40 chromosomes	Frequency of F_1 seedlings with 41 chromosomes
Hark	x	A73-T23-5	9	1
Hark	x	A73-T23-18	6	4
Hark	x	A73-T25-2	6	4
Hark	x	A73-T25-13	8	2
Hark	x	A73-T33-6	4	1
Hark	x	A73-T33-9	4	1
Hark	x	A73-T33-11	3	2
Hark	x	A73-T33-13	3	2
Hark	x	A73-T33-16	5	0

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3. A new mutation for sterility*

In our genetic studies of $\underline{st}_4$ (T258) we routinely harvest seeds from the near-sterile plants ($\underline{st}_4$ $\underline{st}_4$) and study the progeny. Near-sterile plant number 3008-1, found in 1970, had one very small seed, which was subsequently planted in summer 1971. A chromosome count was not obtained from this plant (A71-T48), but it was highly sterile as judged by I_2KI pollen staining; however, it produced four seeds. The pollen from A71-T48 was not typical of the $\underline{st}_4$ sterile. It had large, dark-staining pollen grains instead of the smaller, collapsed, non-starch-filled pollen found in $\underline{st}_4$ steriles. The pollen grains of A71-T48 seemed to have general characteristics of pollen produced by $\underline{ms}_1$ plants (Brim and Young, 1971). The line carrying the $\underline{ms}_1$ gene, however, was not grown at Ames, Iowa prior to 1971.

In 1972, all four seeds from A71-T48 were each determined by root tip squash preparations to have 40 chromosomes and were transplanted to the field.

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Of the three survivors, one was completely fertile and produced many seeds (A72-T28); the other two plants (A72-T30 and A72-T31) were highly sterile with sterility phenotypically identical to the A71-T48 plant.

Two crossed seeds (male parent cultivar 'Clark 63') and two outcrossed seeds were obtained from plant A72-T30. One F_1 seed of the Clark 63 cross and one outcrossed seed were grown in the greenhouse in winter 1972-73 and both plants were highly fertile. The results from the F_1 and F_2 generation in summer 1973 are presented in Table 1.

Table 1
Pollen fertility of F_1 and F_2 progeny from a mutant found in the $\underline{st}_4$ sterile

1972 family number	1973 — number of fertile plants	1973 — number of sterile plants		
		$\underline{st}_4$	non-$\underline{st}_4$	χ^2 test
A72-T28 fertile	51	16	24	0.14(9:3:4)
A72-T29 died				
A72-T30 sterile (non-$\underline{st}_4$)				
F_2 (Clark 63 male)	19	0	7	0.05(3:1)
F_1 (Clark 63 male)	1			
F_2 (outcross origin)	22	0	7	0.01 (3:1)
F_1 (outcross origin)	1			
A72-T31 sterile (non-$\underline{st}_4$)	No progeny			

Meiotic studies indicated first division was normal in the non-$\underline{st}_4$ plants, A72-T30 and A72-T31; second division was not studied. Thus, the mechanism responsible for the non-$\underline{st}_4$ sterility could either be operative in second division of meiosis or it could be post-meiotic.

We hypothesized that pollen from 6 F_2 plants (1/16 of 91) from A72-T28 were phenotypically classified as being from non-$\underline{st}_4$ steriles even though genetically the plants were recessive for both genes. Meiosis will be studied from non-$\underline{st}_4$ plants from A72-T28. It should be possible to classify

those plants that are double recessive, both on the basis of asynapsis (desynapsis), and on the appearance of pollen grains.

References

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4. Distribution of canavanine in the genus Glycine and related genera.

Relatives of the soybean in the genus Glycine have been studied by many workers. Immediate kindred in other genera have not been examined for characters of agronomic interest or possible close relationship to the soybean itself. This report is one facet of our study of the soybean and related genera.

The free amino acid canavanine is known primarily from seeds of advanced legume tribes. Absence of canavanine in some species is thought to be due to the loss of ability to produce the compound, and is considered advanced. Since previous surveys have shown canavanine to be a useful marker of other legume groups, we felt it might help evaluate relationships in the Glycine subtribe, the Glycininae, and its parent tribe, the Phaseoleae.

Procedures for detection of canavanine were adapted from Bell (1958).

Canavanine presence-absence, compiled in Table 1, is constant within most subtribes: all sampled Galactiinae contain canavanine; all Cajaninae, Erythrininae, and Phaseolinae lack it. But Glycininae are inconsistent, and the homogeneity of the subtribe may be questioned. Group 3, conventionally including Glycine, is primarily negative, but there are three exceptions: Shuteria, which perhaps better belongs with group 2; Ophrestia (Paraglycine) hedysaroides, anomalous in that genus on morphological bases; and Glycine wightii, exceptional in Glycine, both on cytological and morphological grounds.

These preliminary findings give rise to several considerations:

1) The correlation between canavanine presence or absence, and the morphological characters upon which several subtribes are based, tends to

Table 1

Species of Phaseoleae examined for canavanine

Genera-Species examined[a]	Reaction[b]	Genera-Species examined[a]	Reaction[b]
Cajaninae		Glycininae[c]	
Cajanus (1)	-	Group 1	
Cantharospermum (1)	-	Centrosema (5)	+
Eminia (1)	-	Periandra (1)	-
Eriosema (1)	-	Clitoria (7)	-
Rhynchosia (9)	-	Group 2	
Diocleinae		Cologania (4)	-
Canavalia (5)	+	Amphicarpaea (1)	-
Pueraria (1)	-	Dumasia (1)	-
Galactiinae		Group 3	
Calopogonium (1)	+	Shuteria (1)	+
Galactia (3)	+	Glycine clandestina	-
Erythrininae		Glycine falcata	-
Apios (2)	-	Glycine canescens[d]	-
Erythrina (3)	-	Glycine tabacina	-
Mucuna (4)	-	Glycine tomentella	-
Phaseolinae		Glycine wightii	+
Dolichos (6)	-	Glycine soja	-
Phaseolus (9)	-	Glycine gracilis	-
Strophostyles (1)	-	Glycine max	-
Vigna (4)	-	Teramnus (1)	-
		Ophrestia hedysaroides	+
		Ophrestia radicosa	-
		Pseudoeriosema (1)	-
		Group 4	
		Hardenbergia (2)	+
		Kennedya (9)	+

[a]Numbers in parentheses are for numbers of species tested.

[b]+ = positive; - = negative.

[c]Groups as given by Bentham and Hooker (1865).

[d]The determination for Glycine canescens is dubious: seed viability for these samples is in question.

validate both the significance of these characters and the possible usefulness of canavanine determinations as a marker of relationships. Instances in which the canavanine seems to be 'out of line' should be restudied with respect to the reasons for placing a given species within a certain genus or the affiliation of a genus with a certain subtribe. Such circumstances may, of course, be caused by loss of an ability to produce canavanine among closely related species (or genera), but in other instances, it may be a clue that a casually assumed relationship is faulty.

2) Previous morphological and cytological evidence suggests that the Glycininae and several included genera are neither homogeneous nor natural, and these data support such a contention. Within Glycine, the conclusions of Pritchard and Wutoh (1964) are supported: these authors, on the basis of cytological studies, separated G. wightii (2n = 22,44) from other species of Glycine (2n = 40,80).

3) Species and genera which have traditionally been placed outside the Glycininae may more properly belong within it, and may be related to Glycine. The Galactiinae are particularly suspect for this possibility, based on these findings and others.

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5. The effect of temperature on the variegation of Y^m_{-18}.

In 1951, a variegated plant was found in the cultivar 'Lincoln' at Ames by C. R. Weber. It has been suggested by Peterson and Weber (1969) that this variegation was due to instability at the Y locus (Y^m_{-18}). The purpose of this investigation is to determine the effect of temperature on the Y^m_{-18} locus.

Seeds from families known to be segregating for variegation were

inoculated with Rhizobium japonicum (serotype 110-8T), and planted in 4-inch clay pots containing a sterile 2 soil : 1 peat : 1 sand mixture. Inoculation with Rhizobium was necessary to obtain nodule formation and nitrogen fixation by the soybean plants. The pots were placed in two growth chambers which maintained 65 F and 85 F environments. After all the leaves had fully expanded, they were removed from the plants and were photographed. The number, size, type of mutation, and leaf area were determined from these photographs. Mutated areas and leaf areas were measured with a polar planimeter. For analysis, it was necessary to assign leaflet position within trifoliate leaves. The middle leaflet was assigned position 2; the leaflet to the left, position 1; the leaflet to the right, position 3. The two unifoliates in the analyses are considered a single unit, and the values presented are an average of both values. This average is designated by $\overline{Un}$.

At 65 F, there were more total mutations and more leaf area mutated than at 85 F. The percentage area mutated at 65 F and 85 F differed only slightly, but this may be a result of a difference in growth of plants at 65 F and 85 F. Mutations to yellow were fewer at 85 F than at 65 F, but involved a larger proportion of leaf area. Light green areas constituted a greater proportion of the leaf area at 65 F than at 85 F (Tables 1 and 2).

At 85 F (Tables 2 and 3), leaflet position 2 had the largest percentage of area mutated, and the largest number of yellow and light green areas. These results, however, are not found at 65 F, except in the yellow areas. Comparison of the total number of mutations and total area mutated according to leaflet position showed distinct differences between the values at 85 F and 65 F (Table 3). The values for area per mutation differed only slightly with leaf position and temperature. At 85 F the yellow area per mutation was larger than the area per mutation at 65 F. This may indicate that mutations to yellow occur earlier in the leaf ontogeny at 85 F than at 65 F (Table 1).

The data may be summarized as follows: The lower temperature (65 F) caused an increase in the number of mutations and an increase in the total area mutated compared with the results at 85 F. The total percentage area mutated and area per mutation differed only slightly between temperature treatments and leaflet positions. At 65 F the percentage of light green

Table 1

The effect of temperature on the number of mutations, leaf area mutated, and area per mutation

	65 F	85 F
Number of yellow areas	6,967	2,923
Number of light green areas	8,971	1,838
Total	15,938	4,761
Yellow area $(in.)^2$	75.7	109.8
Light green area $(in.)^2$	372.1	57.7
Total $(in.)^2$	447.8	167.5
Average yellow area	0.010	0.038
Average light green area	0.041	0.031
Total area $(in.)^2$ per mutation	0.028	0.035

Table 2

The effect of temperature on the percent leaf area mutated with reference to leaflet position

	65 F				85 F			
	Leaflet position				Leaflet position			
	Un	1	2	3	Un	1	2	3
% of total yellow area	4.6	1.7	5.0	4.6	13.8	18.0	23.4	9.9
% of total light green area	15.2	25.5	21.4	24.9	8.5	8.2	9.5	8.4
Total	19.8	27.2	26.4	29.5	22.3	26.2	32.9	18.3

Table 3

The effect of temperature and leaflet position on the number of mutations, leaf area mutated, and area per mutation

	65 F				85 F			
	Leaflet position				Leaflet position			
	Un	1	2	3	Un	1	2	3
Number of yellow areas	1025	1525	1961	2456	275	849	973	826
Number of light green areas	1189	2961	3125	1696	375	483	497	483
Total	2214	4486	5086	4152	650	1332	1470	1309
Yellow area $(in.)^2$	16.2	13.7	26.9	18.9	12.3	34.8	42.8	19.8
Light green area $(in.)^2$	52.9	105.9	113.0	100.3	7.4	15.9	17.4	16.9
Total	69.1	119.6	139.9	119.2	19.7	50.7	60.2	36.7
Yellow area per mutation $(in.)^2$	0.02	0.01	0.01	0.01	0.04	0.04	0.04	0.02
Light green area per mutation $(in.)^2$	0.04	0.04	0.04	0.04	0.02	0.04	0.04	0.03
Total area $(in.)^2$ per mutation	0.03	0.03	0.03	0.03	0.02	0.04	0.04	0.03

leaf area was greater than the percentage at 85 F. Conversely, the yellow areas constituted a larger percentage of the leaf at 85 F than at 65 F.

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1. Seed protein percentage and sulfur-containing amino acid contents in wild soybean (Glycine soja Sieb. and Zucc.) strains native in Japan.

Japanese cultivated soybeans (G. max (L.) Merrill) have been known as protein-rich. However, as the world protein malnutrition problem has been urged to be solved, the development of much higher protein strains is considered to be an indispensable task for soybean breeders. Since the hybridizations of G. max x G. soja (= G. ussuriensis) by Williams (1948) and Weber (1950), G. soja has been regarded as a promising protein gene source in breeding of the G. max varieties with high protein. However, little information is available for the qualitative aspect of G. soja protein. The authors et al. (1972) have already published about the amino acid composition of the species, along with the other Glycine species. Subsequently, the present paper aims to elucidate the inter-strain variability of sulfur-containing amino acid contents in G. soja seed protein.

Twenty-nine G. soja strains were collected from various places of Japan in 1969 and grown in pots at Morioka, Iwate-ken, in 1970, including 8 representative G. max varieties as control. Based on morphological differentiation, the 36 strains were separately harvested and exploited for subsequent chemical analyses. From the seed meal of each strain, protein

percentage (N x 6.25) and sulfur-containing amino acid contents (g/16gN) were determined with two replications by macro-Kjeldahl method and microbioassay, respectively.

The average, maximum, and minimum values of protein percentage and sulfur-containing amino acid contents were indicated in Table 1. As the result of variance analyses, the significant inter-strain differences were indicated for protein percentage, cystine, and cystine plus methionine contents in G. soja. However, it should be strongly emphasized that G. soja generally shows not only higher protein percentage but also higher sulfur-containing amino acid content than G. max does. In addition, although not so distinctive, the protein percentages in G. soja strains slightly decreased with descending latitude of the places where they were originally collected. Similar tendency was noticed concerning sulfur-containing amino acid content, especially the cystine content.

The correlation coefficients between protein percentage and sulfur-containing amino acid content were not significant, i.e. 0.09 for methionine vs., 0.16 for cystine vs., and 0.09 for methionine plus cystine vs. protein percentage, respectively.

The authors et al. (1972) compared the amino acid composition of seed protein among the 6 Glycine species. As a result, no conspicuous differences were observed among the 3 species, G. max, G. gracilis, and G. soja, which belong to the same subgenus Soja. However, in G. max protein, likewise in the other leguminous seed protein, sulfur-containing amino acids are preferred to nutritionally limiting ones. Therefore, in the successful development of G. max varieties with higher protein by interspecific hybridization using G. soja, it would be critical to verify the superiority or non-inferiority for sulfur-containing amino acid content of G. soja to G. max. As was apparently proved in this paper, G. soja is just the case. Moreover, as the G. soja strains tested had been somewhat widely differentiated for protein percentage and sulfur-containing amino acid content even in natural condition, the selection of G. soja strains most suitable for protein breeding would be considered probably to be efficient and also prerequisite. In addition, the geographical distribution for these characters might offer a useful key in the collection and selection program of G. soja strains native in Japan.

Table 1

Protein percentage and sulfur-containing amino acid contents found in the G. soja strains and the G. max varieties in Japan

		Protein* (%)	S-containing amino acid (g/16gN) Methionine	Cystine	Met. + Cys.
G. soja	collected from the northern districts (n_1 = 16)				
N=36 ($=n_1+n_2+n_3$)	Max.	48.2	1.02	1.15	2.15
	Avg.	45.5	0.95	1.04	1.99
	Min.	42.9	0.86	0.88	1.80
	collected from the middle districts (n_2 = 12)				
	Max.	48.1	1.01	1.10	2.08
	Avg.	43.9	0.96	1.02	1.98
	Min.	40.7	0.90	0.84	1.80
	collected from the southern districts (n_3 = 8)				
	Max.	47.4	1.04	1.01	1.97
	Avg.	44.5	0.95	0.92	1.87
	Min.	41.2	0.88	0.73	1.68
G. max N=8	Max.	40.6	0.88	1.02	1.89
	Avg.	39.6	0.81	0.98	1.79
	Min.	37.5	0.73	0.95	1.68

*Not moisture-free basis.

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1. A note on a soybean mutant.

Seeds of S.J.2, a Thai soybean variety, were treated with gamma rays of a cobalt source in five different doses: 5, 10, 15, 20 and 30 krad, respectively.

In M_2 generation, yellow seedlings appeared in the treated materials, with the frequency ranging from 0.20 to 0.70%. Two different types of yellow seedlings were observed. The first type: the seedlings had both yellow cotyledons and yellow first single leaves. They died at the seedling stage. The second type: only the first single leaves were yellow, but turned green toward maturity.

Line Number 41-10 was obtained from the second type. Its plant height at maturity is somewhat shorter than that of the mother variety. This mutant has 44% protein (on dry matter basis), about 2% higher than that of the mother variety.

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1. An attention to the heritability of pod dehiscence as affected by environment.

Pod dehiscence or shattering is an agronomic character of importance in breeding soybeans adaptable to machinery cultivation. Caviness (1969) had presented heritability estimation of pod dehiscence in four crosses between varieties in the United States and the wild soybean, and the values in broad sense in F_2 generation were very high (over 90%). The author (Nagata, 1974) has reported results of observations of pod dehiscence under

different conditions with special regard to the moisture contents of plant parts, especially of seeds, and concluded that pod dehiscence was affected greatly by environment and year with reference to the meteorological conditions. The degrees of pod dehiscence seemed to be different between those in marine climate in Japan and in continental climates in the United States and other countries.

The author had tested the degrees of pod dehiscence in three crosses between an American variety resistant, and the Japanese varieties susceptible to the pod dehiscence during several years.

In general, heritability of pod dehiscence in our experiments in Japan was estimated to be very low, especially in the field (Table 1). Such a difference between those in field and in the glass-house (where pods were layed in bags of translucent parchment paper) was more significant in later segregating generations though it was not fully coincident among the crosses.

In our country, there is frequent rain and high humidity, and the appearance of the nature of pod dehiscence of the variety or strain is very variable. In field, the area for experiment becomes larger with advancement of generation, and so environmental variance becomes larger, especially in the humid and rainy climate in our country. In contrast to that in field, the environmental variance is capable of being limited in the glass-house where many strains or individuals are layed under comparatively uniform condition without the effect of rain. It should, however, be noted that the tests in the field are more practical for breeding soybeans than those in the glass-house.

In Japan, breeding of non-dehiscent varieties has not advanced up to the present. Because of this problem, the genetic differences between pod dehiscence resistant and susceptible varieties are not as great in Japan as in countries of continental climate. Cultivation of soybeans in our country was the system of hand labor of farmers in which pod dehiscence was not a problem for harvesting, but now harvest is being mechanized with small or medium-size harvesters adaptable to Japanese agriculture. Thus, pod dehiscent property of soybeans is becoming important for the agronomists in experiment stations.

It should be emphasized herein that testing pod dehiscence of soybeans ought to be carried on with consideration of the climatic or meteorological

conditions of the land or season of cultivation, especially in Japan and countries in Southeast Asia of marine climate.

Table 1

Estimate of heritability in the broad sense in F_2 generation from the cross, Tokachi Nagaha x Harosoy

V_E	In field	In glass-house
V_{F_1}	23.04%	37.50%
V_{PF_1}	30.04%	48.53%

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1. Research note from Applied Genetics Laboratory.

Wide variations of locally grown farmers' varieties were observed in Korea. The majority of varieties currently grown by farmers are unnamed and succeeded from their ancestors. The gene collection is urgently needed for the present varietal improvement and also to prevent the erosion of gene sources built up many centuries in this land. Mutation breeding and an establishment of soybean gene pool are now under progress.

Shin Han Kwon

Editor's note

Dr. Kwon has sent 377 of these farmers' varieties to be added to the Germplasm Collection at Urbana, Illinois. These along with 152 recently received from the Office of Rural Development at Suwon and 73 collected by R. L. Bernard while in Korea in fall 1972 total approximately 600 new introductions of land varieties from Korea. The great majority are of maturity group IV

with some III's and V's. Seed will be available for distribution after the 1974 harvest from R. L. Bernard, U.S. Regional Soybean Laboratory, Urbana, Illinois 61801.

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1. Exploitation of leaf mosaicism for determination of allelic relationship in Glycine max.

Glycine max (L.) Merrill (soybean) is said to have at least 18 loci responsible for the development of chlorophyl (Bernard and Cremeens, 1970). One of these, $\underline{y}_{11}$, discovered by Weber and Weiss (1959), is characterized by the development of golden yellow color of the leaves and stem in homozygous ($\underline{y}_{11}\underline{y}_{11}$) combination. The heterozygous plants are light green and differ from the $\underline{Y}_{11}\underline{Y}_{11}$ homozygotes which have normal, dark green color. The two simple and the first compound leaves of the heterozygous plants are dotted with dark green, yellow and twin or double (dark green-yellow) spots. Origin of some of these spots, particularly those of twins, has been attributed to the process of somatic crossing over (see Vig and Paddock, 1968; Vig, 1971, 1972, 1973a,b). Also, the frequency of these spots can be increased several fold by treating the seed with chemicals, e.g. caffeine, mitomycin C, etc.

Another gene, $\underline{y}_9$, in homozygous recessive $\underline{y}_9\underline{y}_9$ combination produces a bright greenish yellow leaf and stem color (Probst, 1950). $\underline{Y}_9\underline{y}_9$ or $\underline{Y}_9\underline{Y}_9$ plants are dark green. Considering the two genes and their alleles so far discussed, one gets the following combinations: $\underline{Y}_9$ - $\underline{Y}_{11}\underline{Y}_{11}$ = dark green; $\underline{Y}_9$ - $\underline{Y}_{11}\underline{y}_{11}$ = light green; $\underline{Y}_9$ - $\underline{y}_{11}\underline{y}_{11}$ = yellow, lethal; $\underline{y}_9\underline{y}_9\underline{Y}_{11}\underline{y}_{11}$ = bright greenish yellow; $\underline{y}_9\underline{y}_9\underline{y}_{11}\underline{y}_{11}$ = not known.

Traditionally, relationships between genes (or alleles) can be studied by raising hybrids like $\underline{Y}_9\underline{y}_9\underline{y}_{11}\underline{y}_{11}$ and analyzing the segregating populations. However, we decided to make use of induced somatic mosaicism for such a study. The reasoning is as follows: if $\underline{y}_9\underline{y}_9\underline{Y}_{11}\underline{Y}_{11}$ plants are treated with a known recombinogen or mutagen (say caffeine or mitomycin C) one should

expect a mutation of the gene $\underline{y}_9$ to $\underline{Y}_9$, thus changing the color of the affected colony of cells to dark green. Another possible mutation of $\underline{Y}_{11}$ to $\underline{y}_{11}$ will not alter the phenotype of the resulting $\underline{y}_9\underline{y}_9\underline{Y}_{11}\underline{y}_{11}$ colony. If, on the other hand, genes $\underline{y}_9$ and $\underline{y}_{11}$ are alleles, rather than occupying two loci, one may also expect some dark green sectors ($\underline{Y}_9\underline{Y}_{11}$), considering that genotype of bright greenish yellow plant is $\underline{y}_9\underline{Y}_{11}$ ($\underline{y}_9$ and $\underline{y}_{11}$ are alleles) and not $\underline{y}_9\underline{y}_9\underline{Y}_{11}\underline{Y}_{11}$. In the latter case, however, one may also expect a few yellow ($\underline{y}_9\underline{y}_{11}$) spots if $\underline{Y}_{11}$ mutates to $\underline{y}_{11}$ (and if $\underline{y}_{11} > \underline{y}_9$). In case of $\underline{y}_9\underline{y}_9\underline{Y}_{11}\underline{Y}_{11}$ genotype, no yellow spots are possible unless one postulates an unexpected double mutational event involving both $\underline{y}_{11}$'s.

In one series of experiments, the seeds of Clark x T135 (segregating for $\underline{Y}_9\underline{y}_9$), T135 ($\underline{y}_9\underline{y}_9$), L65-1237 ($\underline{Y}_{11}\underline{y}_{11}$ segregant) and T219 ($\underline{Y}_{11}\underline{y}_{11}$ segregant) were planted without pretreatment. In all cases, all three types of spots previously seen on $\underline{Y}_{11}\underline{y}_{11}$ plants were observed. The color of the spots on the $\underline{y}_9\underline{y}_9$ plants resembled closely the color of $\underline{Y}_{11}\underline{y}_{11}$ leaves. In another experiment, seeds of T219, L65-1237, T135, Clark x T135, T136 ($\underline{y}_6\underline{y}_6$) and Clark x T136 (segregating for $\underline{Y}_6\underline{y}_6$) were planted with and without treatment with mitomycin C. The control $\underline{y}_9\underline{y}_9$ had a few spots of all three types found on $\underline{Y}_{11}\underline{y}_{11}$ leaves. The frequency in the treated material went up by 2 to 6 times in case of both $\underline{y}_9\underline{y}_9$ and $\underline{Y}_{11}\underline{y}_{11}$ plants. No spots, however, were observed on the $\underline{y}_6\underline{y}_6$ plants.

A third set of experiments was performed using $\underline{y}_9\underline{y}_9$ (T135) seed soaked in water, or solution of mitomycin C, or caffeine. Spot frequencies per leaf ranged from 0.56 for water-soaked (control) material, to 0.94 for 0.002% mitomycin (18 hr) and 9.49 for 0.1% caffeine (18 hr). All three types of spots were found in almost equal frequencies. Several more experiments gave parallel results.

The data reported above raise some interesing points. First, the appearance of yellow spots on the T135 leaves indicates a relationship between $\underline{Y}_{11}$, $\underline{y}_{11}$ and $\underline{Y}_9$, $\underline{y}_9$. The most convincing solution to this puzzle appears to consider $\underline{Y}_{11}$ and $\underline{Y}_9$ as the <u>same</u> gene and $\underline{Y}_9$ (or $\underline{Y}_{11}$), $\underline{y}_9$, $\underline{y}_{11}$ as alleles. Thus $\underline{y}_9$ in $\underline{y}_9\underline{y}_9$ can mutate to either $\underline{Y}_9$ (= $\underline{Y}_{11}$) or to $\underline{y}_{11}$. This explains the origin of two types of single spots on T135 leaves. Thus $\underline{Y}_9$ (= $\underline{Y}_{11}$) and $\underline{y}_{11} > \underline{y}_9$, but $\underline{Y}_9$ (= $\underline{Y}_{11}$) is incompletely dominant over $\underline{y}_{11}$.

Another problem is the explanation of the origin of twin spots on the $\underline{y_9 y_9}$ leaves. It requires a complementary exchange between the two $\underline{y_9}$ genes producing $\underline{Y_9}$ (= $\underline{Y_{11}}$) and $\underline{y_{11}}$ in a single step. I wish to advance the following hypothesis: the gene $\underline{Y_9}$ is composed of a DNA segment which carries two tandem repeats. An addition of another repeat causes the partial loss of activity of the final product (the protein produced). This was $\underline{y_9}$. A loss of one of the repeats in $\underline{Y_9}$ causes almost the total loss of activity of the product. This is $\underline{y_{11}}$. In a somatic cell with some arrangement for interaction between homologous chromosomes, there is every chance of a given repeat segment loosely pairing with any other similar segment found in recombination required by somatic crossing over. Such unequal crossing over in $\underline{y_9 y_9}$ homozygote will produce $\underline{y_9 Y_9}$-$\underline{y_{11} y_9}$ cells which will express as a double spot colony. This hypothesis is also compatible with spots on $\underline{Y_{11} y_{11}}$ plants.

In view of the above, I suggest that possible allelic relationship between $\underline{Y_9}$ and $\underline{Y_{11}}$ be explored, but the question of redesignation of $\underline{Y_9}$ and $\underline{Y_{11}}$ be postponed until further evidence is available from crosses and segregating populations.

The lack of yellow spots on other genes tested may indicate non-allelic relationship with $\underline{Y_9}$ series.

The seed for all these studies was provided by R. L. Bernard. I am grateful for his generosity.

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1. Soybean rust and soybean rust research.

During May 1973 I visited scientists in Australia, Indonesia, Thailand and Taiwan to discuss the current status of soybean rust and soybean rust research. Each of my hosts expressed a desire to be informed of what I learned elsewhere on my trip. The following informal summary is an attempt to comply with these requests.

Australia:

Major soybean growing areas: Almost all of the soybeans grown in Australia are found in Queensland and New South Wales, with very minor acreages in northern Victoria. The area sown to soybean in 1973 was about 28,350 hectares in Queensland and about 8,100 hectares in New South Wales. Important growing areas in Queensland include The Darling Downs; the South Burnett region (Kingaroy, Nanango, Wondai, Murgon); the Lockyer, Fassifern and Brisbane River Valleys; the Atherton Tablelands; and the region around Bundaberg. In New South Wales, soybeans are found in the Northwest Region (Quirindi, Gunnedah, Narrabri, Wee Waa, Moree, Walgett); the Central West Region (Dubbo, Narromine, Trangie); the Riverina Region (Deniliguin, Hay, Leeton); Cawra and Conowindra west of Sydney; and the North Coast (Coffs Harbour, Lismore, Casino).

Rust occurrence: Although Phakopsora pachyrhizi had been first reported in Australia in 1934, it apparently did not become serious on soybeans until 1970 when it strongly attacked plantings at Redland Bay, Queensland. Since then it has been found yearly at Redland Bay. Also in Queensland it has been reported from Gatton, Toogoolawah, Brookstead (ca. 120 miles inland from Brisbane), Nambour, and the Atherton Tablelands (where it may be a limiting factor to soybean production). In New South Wales it has been found at Lismore, Casino and Coffs Harbour, with serious damage being reported in May of this year at Coffs Harbour.

In Australia, P. pachyrhizi has also been reported on G. clandestina and G. wightii. It is thought that rust may be found year round on certain pasture legumes in northern Queensland and that this reservoir may be the primary source of inoculum infecting soybean plantings.

Workers and research underway: Lester W. Burgess and Robert Keogh, Dept. of Plant Pathology and Agricultural Entomology, University of Sydney, Sydney 2006, New South Wales, Australia.

Keogh is a post-graduate student working toward the M.Sc.Agr. degree under Burgess. His thesis title is "The biology of Phakopsora pachyrhizi." Current emphasis is on screening Australian legumes for susceptibility to rust and on details of infection and establishment processes. Keogh's work to date has extended the list of genera and species known to be susceptible to P. pachyrhizi.

The following scientists at the University of Sydney have a general interest in soybean rust because of their specific interest in soybean as a crop: Owen Carter, D. R. Laing, P. Michael and K. S. McWhirter. McWhirter currently maintains the University's soybean germ plasm collection.

D. E. Byth, Dept. of Agriculture, University of Queensland, St. Lucia, Queensland 4067, Australia. Byth's work involves soybean breeding and an irradiation program aimed at inducing rust resistance or tolerance. His material is severely challenged each year by natural rust infection at Redland Bay. In 1970 his entire germ plasm collection was observed for rust reaction. All varieties were susceptible. Since then he has introduced PI 200.451 (maturity group VII), PI 200.490 (maturity group VII), and PI 200.492 (maturity group VII) from the U.S. and has made crosses with them and selected Australian varieties. The progenies of these crosses are being challenged by rust. Byth is currently at the University of Guelph, Ontario, Canada on a year's sabbatical leave from the University of Queensland.

Helen Ogle, Plant Pathology Section, Department of Primary Industries, Indooroopilly, Queensland, Australia. Ogle anticipates initiation of research on P. pachyrhizi in the near future.

Indonesia:

Major soybean growing areas: The bulk of Indonesia's soybeans are grown on the island of Java. Following are estimates of the area (in

hectares) planted to soybeans in Java: West Java — 27,000; Central Java — 127,000; Special Territory of Jogjakarta — 25,000; East Java — 388,000. The total area planted to soybeans elsewhere in Indonesia is about 99,000 hectares.

Rust occurrence: Soybean rust occurs on soybeans and Pachyrhizus bulbosus in West Java and is of concern there. Ir. Triharso has surveyed for rust in the Special Territory of Jogjakarta but has not found it there. To date I have no information on the soybean rust situation in East Java or elsewhere in Indonesia. I would greatly appreciate receiving information on this point.

Workers and research underway: Ir. Triharso (plant pathologist) and Soenjoto Djojodirojo (plant breeder), University of Gadjah Mada, Jogjakarta, Indonesia are both alert to the possibility of rust and will undertake work on it, should it become a factor in Central Java. An INTSOY* nursery will be planted near Jogjakarta.

Fred Rumawas, Director of Research, Institute Pertanian Bogor, Bogor, Indonesia is observing the behavior of soybean rust in his nurseries at Darmaga. Rumawas is collecting soybeans from all parts of Indonesia in order to characterize local varieties. In addition, accessions from other countries are being assembled and tested. An INTSOY nursery is also being planted here.

Russel D. Freed, a staff member of IRRI**, currently working on multiple cropping problems at Central Research Institute for Agriculture (Lembaga Pusat Penelitian Pertanian), Bogor, has a general interest in rust as a factor affecting soybeans in multiple cropping schemes.

Thailand:

Major soybean growing areas: The total soybean area in Thailand is estimated to be 53,055 hectares. The province of Sukhothai has about 60% of this total. Other important areas are Chiang Mai and Nakhonsawan. Some soybeans are also grown in Chaiyaphum and Nakhonrajasima in the Northeast Region of Thailand.

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Soybeans are planted twice a year in Thailand; a dry season planting and a rainy season planting. The dry season planting is made in paddies from January to April, following rice harvest, and requires irrigation water. This practice is frequently followed in the Chiang Mai area, which has an adequate supply of irrigation water available. During the rainy season, plantings may be made from May to November. The time of planting varies with location and with cropping sequence. INTSOY nurseries will be planted at Khon Kaen, Chiang Mai, Chainat, and Farm Suwan.

Rust occurrence: Soybean rust is said to be the most destructive disease of soybeans in Thailand. It is found in all of the major soybean growing areas and is most serious during the rainy season months of September and October.

Workers and research underway: Prateung Sangawongse (plant pathologist), Plant Pathology Section, Department of Agriculture, Ministry of Agriculture, Bangkok, Thailand. Prateung is studying the biology of the soybean rust fungus and is testing chemicals for rust control in the major growing areas. No chemical spray treatments as yet have been found to be economically feasible under Thai conditions. Prateung's observations indicate that S.J.2 is more tolerant of rust than S.J.1.

Sman Keoboonrueng (plant pathologist), Agricultural Center NE, Khon Kaen, Thailand. Some of the work at the Agricultural Center NE is directed toward breeding and selection of adapted soybeans producing high protein beans that could be used as cattle feed. Soybean rust has not been found at Khon Kaen, although it has been reported from areas further east. Should it appear at Khon Kaen, Sman would undertake research on the disease.

Mr. Sunan (Director), Kijoro Kokobun (soybean breeder) and Yoshimitsu Tanimura (soybean breeder), Mae Jo Agricultural Experiment Station, Chiang Mai, Thailand. Breeding for adapted varieties with rust resistance is in progress. The rust resistant parent being utilized is the Taiwan variety Tainung 4 (designated at the Mae Jo Station as 64-104). Tainung 4 derives its rust resistance from PI 200.492.

Taiwan:

Major soybean growing areas: The major soybean growing districts in Taiwan with the estimated area (expressed as hectares) devoted to soybeans

are: Pingtung (27,000); Kaohsiung (6,000); Hualien (3,000); and Chiayi (1,000). Another 3,000 hectares of soybeans are planted elsewhere to make a total of about 40,000 hectares.

Spring, summer, or fall planting of soybeans may be made. Spring plantings are made from mid-February to mid-March, summer plantings in June to July, and fall plantings from mid-September to mid-October. Approximately 75% of the soybean crop is fall-sown.

Rust occurrence: Soybean rust is considered the major soybean disease in Taiwan. It is found throughout the island every year. Rust is reported more severe on the spring-sown and autumn-sown crops than on the summer-sown crop. High severities are attained at an earlier crop development stage in the spring and autumn crops than in the summer crop.

Rust has been an economic factor in soybean production for well over a decade and the disease and pathogen have been investigated by workers in the Taiwan Agricultural Research Institute (TARI), several District Agricultural Improvement Stations (DAIS), and Universities. Reports concerning chemical control of rust; environmental factors affecting spore germination, penetration, development and sporulation; the demonstration of physiologic races, etc., are in the literature.

Breeding for rust resistance has been in progress since about 1961, using PI 200.492 (maturity group VII) as a resistant parent. Tainung 3, Tainung 4, and Kaohsiung 3 are released varieties that carry rust resistance. (I personally tend to characterize their resistance as "field resistance." Pustules that develop on them are of an infection type similar to that produced on susceptible varieties, but in the field the degree of rustiness is markedly lower than that on varieties like susceptible Shih-Shih growing adjacent to them.)

Workers and research underway: Kuo-Lein Chan (soybean specialist), Taiwan Agricultural Research Institute, Roosevelt Road, Taipei, Taiwan, Republic of China. Chan worked on the development of Tainung 3 and Tainung 4 and is continuing work in breeding for resistance to rust. Currently he also has underway experiments designed to yield quantitative information on losses attributable to P. pachyrhizi. Chan is also investigating the chemical control of rust. In estimating rust severity, he utilizes a photographic scale illustrating 6 degrees of rustiness.

Ying-Chuan Lu (Head, Dept. of Agronomy) and Kuo-Hai Tsai, National Chung-Hsing University, Taichung, Taiwan, Republic of China. Lu and Tsai have obtained rust resistant lines of soybean from seed irradiated with gamma radiation. This work is to be published in a forthcoming issue of SABRAO. If the resistance is stable, it will markedly increase the number of available genotypes with rust resistance.

Charles Y. Yang (Head, Division of Plant Pathology) and S. Shanmugasundaram (breeder and coordinator of soybean investigations), Asian Vegetable Research and Development Center (AVRDC), P.O. Box 42, Shanhua, Tainan 741, Taiwan, Republic of China. Soybean is one of six crop plants under investigation at the AVRDC. Shanmugasundaram (Sundar) is assembling soybean germplasm from throughout the world. Yang is initiating a broad research program on all aspects of soybean rust.

Relevant rust research by U.S. workers:

In 1961, the entire USDA soybean germplasm collection was planted in Taiwan and screened for rust resistance. This was a cooperative effort involving various scientists in Taiwan, E. E. Hartwig (Research Agronomist, USDA, ARS, Soybean Production Research, Delta Branch Experiment Station, Stoneville, Mississippi 38776), and R. L. Bernard (Research Geneticist, USDA, ARS, U.S. Regional Soybean Laboratory, 160 Davenport Hall, Urbana, Illinois 61801). The only accessions found to possess marked resistance were PI 200.490 (maturity group VII) and PI 200.492 (maturity group VII). These two accessions had been obtained from Shikoku Islands, Japan, in 1952. As mentioned above, PI 200.492 has been utilized in Taiwan to produce Tainung 3, Tainung 4, and Kaohsiung 3. Bernard and Hartwig made crosses between some U.S. commercial varieties and PI 200.492. The progenies of these crosses have been carried through several generations but to date have not been screened for rust reaction.

In 1970 and 1971, the U.S. germplasm collection was planted at Pantnagar (Nainital), Uttar Pradesh, India to screen for resistance to the yellow mosaic virus (yellow virus) transmitted from mung bean to soybean by white fly (Bemisia tabaci). Soybean rust appeared in the plots in both years. Hartwig was able to make rust observations both in 1970 and 1971.

In the autumn of 1972 Bernard made extensive collections of G. ussuriensis (G. soja) in Korea and Japan. Perhaps genes for rust resistance are present in this material.

Research on the biology of P. pachyrhizi and the etiology and epidemiology of soybean rust was begun in 1972 at the Plant Disease Research Laboratory, USDA, ARS, NER, P.O. Box 1209, Frederick, Maryland 21701. Currently, work is underway in specially designed and operated containment facilities with cultures of rust obtained from four rather widely separated geographical regions: Australia, India, Indonesia, and Taiwan. Spore germination, penetration, development within the host, and sporulation are being studied under controlled environment conditions. The behavior of each of the four cultures on U.S. commercial varieties, accessions with reputed rust resistance, and various legumes is being compared. Studies designed to provide information on rates of increase and yield loss attributable to rust have also been initiated. Plant pathologists investigating soybean rust at PDRL are K. R. Bromfield, M. A. Marchetti and J. S. Melching.

Workers in additional countries:

In a recent letter, Rudy S. Navarro (plant breeder), University of the Philippines, College of Agriculture, College, Laguna, Philippines, indicated that in the period 1967-1971 varieties Wayne, TK-5, K.E. 32 and Taichung E-31 and certain lines arising from the breeding program at UPCA were resistant to rust in the Philippines. However, during the period Nov. 1972 to Jan. 1973, all of these varieties and selections became heavily infected, leading to the conclusion that a new pathogenic race became prevalent.

Other workers with more than a casual interest in soybean rust are: Richard M. Lantican, Agronomy Department, University of the Philippines, College of Agriculture, College, Laguna, Philippines; F. C. Quebral, Plant Pathology Department, University of the Philippines, College of Agriculture, College, Laguna, Philippines; William M. Brown, Jr., C.P.O. Box 143, Seoul, Korea; Hoo Sup Chung, College of Agriculture, Suwon National University, Seoul, Korea; P. N. Thapliyal, Department of Plant Pathology, College of Agriculture, G. B. Pant University of Agriculture and Technology, Pantnagar, Dist. Nainital, U. P., India.

I am certain there are other workers doing research on soybean rust and/or its causal agent P. pachyrhizi. It would be greatly appreciated if you send me the names and addresses of these scientists.

Miscellaneous:

1) Rust pustules that I saw on leaves in both Java and Thailand were dark colored and did not look "powdery." I got the impression that they were being attacked by a bacterial hyperparasite. Does anyone have any information on this? Actually, it was frequently difficult for me to distinguish between bacterial pustule lesions and rust lesions in Java and Thailand. This was in marked contrast to the situation in Taiwan where the pustules were "reddish tan" and quite pulverulent in appearance.

2) In my notes I recorded, without further elaboration, that HY2217 from the Philippines carries resistance to rust. Any further information on this?

3) S. Moin Shah, Chief Pathologist, Department of Agriculture, Khatmandu, Nepal informed me that Uromyces vicae-fabae attacks soybeans in Nepal. Is there any other evidence for this?

Hope you find useful information in this summary. Please keep me informed on the soybean rust situation in your respective area of the world.

K. R. Bromfield

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Department of Agronomy
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1. Soybean tissue culture studies.

Tissue culture methods may benefit soybean breeders if whole plants can be differentiated from aneuploid, mutated, fused, or haploid cells. However, in order to realize this potential, it must be possible to derive plantlets from previously undifferentiated tissues — and ultimately from masses of callus cells. This report summarizes the information we obtained concerning adventitious budding from soybean tissues (Kimball and Bingham,

1973), early stages of embryo formation within masses of callus cells, and actual differentiation of plantlets from callus tissue.

'Dunn' was selected for initial studies, with other cultivars tested later. Modifications of Miller's (1965) and Gamborg's (1966, 1968) media were used for most studies. All experiments were carried out aseptically, using either semi-solid or liquid media. Cultures were kept under about five Klx continuous fluorescent light at 28 C. Several replications of each treatment were examined.

Initial studies indicated that from 2 to 8% of the uppermost hypocotyl sections and basipetal cotyledon sections produced buds from parenchymatous somatic cells, but root tips, root-hypocotyl transition zone sections, and cotyledon mid- and tip-sections did not respond. Bud differentiation was polarized, with shoots developing from the acropetal cut surface of the hypocotyl sections and from the basipetal cut surface of the basipetal portion of the cotyledons. Gamborg's medium (1966) with 15% coconut milk (or 0.5 mg/liter 2-isopentenyl adenine) and 0.5 mg/liter IAA; and Miller's medium (1965) with 0.5 mg/liter kinetin (or 2-iP) and 0.5 mg/liter IAA, were most conducive for such adventitious budding. Several cultivars produced adventitious buds (Table 1), hence the phenomenon is not overly variety-specific.

Generally, there is an inverse relationship between callus formation and adventitious budding, with 2,4-D causing the most callus but no budding, and IAA causing the least callus formation but the most bud differentiation. Addition of about 0.03 mg/liter 2,4-D to any of the above-mentioned media caused optimum callus and shoot development, but over 0.05 mg/liter 2,4-D inhibited bud formation.

Free cell cultures from 'Dunn' callus were also evaluated for morphogenetic trends. Hypocotyl and cotyledon sections were placed on Gamborg's B5 medium (1968) with 0.5 mg/liter IAA and kinetin for two weeks to form callus. The newly formed callus was then transferred to a liquid medium (Miller, 1965) with 0.5 mg/liter IAA and kinetin, and 1.0 mg/liter 2,4-D. After two weeks on a shaker table, the original callus had given rise to a cloudy suspension of free-floating cells. Microscopic examination of cell suspensions, four weeks in shake culture, revealed chains and clusters of

cells similar to filamentous and globular-phase proembryos observed in normal embryogenesis. Compact spheres of cells began to accumulate at the bottom of culture flasks after five to six weeks, often 500 to 600 from an initial 2mm hypocotyl section. Two weeks after these spheres began to accumulate, about 95% of them developed a single root, and soon recallused. Of the spheres that failed to develop rootlets, about 20% appeared to have the external morphology of proembryos (net: about 1% of spheres) including a cotyledonary-like cleft at one end and an elongated axis and having vascular differentiation within.

Similar results were obtained with the cultivated varieties 'Dunn', 'Wayne' and 'Hardee' and plant introductions of G. tabacina and G. ussuriensis (now designated G. soja). The low frequency of heart-phase proembryos probably reflects the inability of globular-phase proembryos to develop organized apical and leaf meristems when exposed to the high auxin levels necessary to produce cell suspensions.

Several different cultures have actually differentiated shoots from callus clumps, but at a low frequency. 'Dunn' embryos were cultured on Gamborg's B5 medium, the developing callus growth being subcultured on similar media after 15 weeks. Seven weeks later, the calli were broken up and subcultured again onto new B5 media. After another four weeks, leaf-like structures were noted on one of the subcultures — after a total of six months of culture on the B5 media. Shoots and plantlets have also developed from callus tissue of Glycine tabacina after culturing apices on the above-mentioned B5 medium. Roots developed after 7 weeks, followed by a cluster of five shoots that developed from a subsurface root or rhizome-like structure seven weeks later.

In summary, it is now known that soybean can produce adventitious buds from tissue sections; that under shake-culture, free cells can be induced to divide and organize into proembryoid-like structures; and that, under special conditions, adventitious shoots develop from masses of callus cells. The task at hand now is to refine the above mentioned techniques to produce consistent differentiation from callus.

Table 1

Differentiation of adventitious buds

Cultivar	Plant material cultured	
	Hypocotyl	Cotyledon
Dunn	+	+
SRF 307P	+	+
Verde	+	+
Corsoy	+	-
Ransom	+	-
Anoka	-	+
Dunfield* (T214)	-	+
Lincoln* (T212)	-	+
Richland* (T213)	-	+
Altona	-	-
Disoy	-	-
Hardee	-	-

*Tetraploids.

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S. L. Kimball
G. L. Cutter
W. D. Beversdorf
E. T. Bingham

V. INDEX OF CONTRIBUTORS

VII. GENETIC STOCKS AVAILABLE

Procedure for Requesting Seeds from the USDA Soybean Germplasm Collection

The USDA maintains a collection of soybean germplasm comprising about 4,000 strains of current and obsolete American varieties, foreign introductions, genetic types, and related species. Seed packets are available for research purposes upon request. The following points are listed to guide you in requesting seeds:

1. Please address requests for early-maturing varieties and PI and FC strains (Maturity Groups 00 to IV), Genetic Types (T-strains), and wild species of Glycine to:

   Dr. R. L. Bernard
   U.S. Regional Soybean Laboratory
   160 Davenport Hall
   Urbana, Illinois 61801
   Tel. 217-333-4639 (FTS 356-1124)

   and requests for late-maturing varieties and PI and FC strains (Groups V to X) to:

   Dr. E. E. Hartwig
   Delta Branch Experiment Station
   Stoneville, Mississippi 38776
   Tel. 601-686-7281, Ext. 230

2. Time of requests:
   Small requests will be filled as soon as possible after receipt. We appreciate advance notice (at least by March 1) on large requests and normally packet these in March-April for planting that season. If you plan to use the seeds at some other time of the year, you should anticipate the need and send us the request by March 1 as we rarely go through the whole collection at other times of the year.

3. Amount of seed:
   a. A standard request is about 50 seeds per packet, but we can easily furnish a smaller number and, if seed supply permits, will also furnish larger amounts. Specify how many you want. If no amount is specified, we will send 50 seeds.

b. Seed counts are only approximate, as we cup the seeds, and only partially compensate for size and germination variation.

c. In the case of named varieties we can sometimes furnish larger amounts, up to a kilogram or so, especially in the case of varieties which we are currently yield testing.

d. The tropical perennial species (all species other than G. max and G. soja) are difficult to grow and reproduce, and normally only a few (5 to 10) seeds will be sent.

4. Lists and reports are available to assist you in selecting and requesting germplasm.

a. Checklists giving name and maturity group. Extra copies are available to use in making requests for large numbers of strains.

1. Groups 00 to IV varieties, 1973.
2. Groups 00 to IV FC and PI strains, 1973.
3. Groups V to VIII varieties and FC and PI strains, 1967.

b. Evaluation reports giving origin of strains and descriptive, agronomic, and seed composition data:

1. Varieties, Groups 00 to IV, 1970.
2. Varieties, and FC and PI strains, Groups 00-0, 1965.
3. Varieties, and FC and PI strains, Groups I-II, 1966.
4. Varieties, and FC and PI strains, Groups III-IV, 1969.
5. Varieties, and FC and PI strains, Groups V-VIII, 1966.
6. Recent varieties and PI additions, Groups 00-IV, 1970.
7. Genetic Type Collection, 1970.

c. List of wild soybeans, Glycine soja.

d. List of backcross isolines of Clark and Harosoy.

5. Before sending in your request, please verify the accuracy of your strain designations and whether they are maintained at Urbana or Stoneville by checking them against a current checklist or evaluation report. We get many requests for nonexistent varieties and PI's and you are in a better position than we are to correctly identify what you want.

6. There is no charge for seed for research purposes.

7. We appreciate knowing the intended use of the seeds in all cases and we must know it in the case of very large requests. We also appreciate receiving copies of publications or other information that you derive from the use of these seeds.

April, 1974.

†Table 1a. List of genes affecting disease reaction in soybeans

Gene	Phenotype	Strain*	Reference
	1. Bacterial pustule		
Rxp	Susceptible	Lincoln, Ralsoy	Hartwig and Lehman, 1951; Feaster,
rxp	Resistant	CNS	1951; symbol assigned here.
	2. Bacterial blight		
Rpg_1	Resistant to race 1	Norchief, Harosoy	Mukherjee et al., 1966.
rpg_1	Susceptible to race 1	Flambeau	
	3. Frogeye leaf spot		
Rcs_1	Resistant to race 1	Lincoln, Wabash	Athow and Probst, 1952 (as Cs);
rcs_1	Susceptible to race 1	Gibson, Patoka, Hawkeye	symbol by Probst et al., 1965.
Rcs_2	Resistant to race 2	Kent	Probst et al., 1965.
rcs_2	Susceptible to race 2	---	
	4. Downy mildew		
Rpm	Resistant	Kanrich	Bernard and Cremeens, 1972.
rpm	Susceptible	Clark, Chippewa	
	5. Phytophthora root rot		
Rps	Resistant	Mukden, Illini	Bernard et al., 1957 (as Ps);
rps	Susceptible	Lincoln	symbol by Hartwig et al., 1968.
rps^2	Resistant to race 1 & susceptible to race 2	FC 31.745	Hartwig et al., 1968.
	6. Cyst nematode		
$rhg_1rhg_2rhg_3$	Resistant	Peking	Caldwell et al., 1960.
Rhg_1, Rhg_2, or Rhg_3	Susceptible	Lee, Hill, c	
Rhg_4	Resistant	Peking	Matson and Williams, 1965.
rhg_4	Susceptible	Scott, c	

†Tables 1a-1g are taken from ASA Monograph No. 16, Chapter 4, "Qualitative Genetics," by R. L. Bernard and M. G. Weiss, and cannot be copied without specific permission from the American Society of Agronomy.

Table 1b. List of genes affecting *Rhizobium* response in soybeans

Gene	Phenotype	Strain*	Reference
$\underline{Rj}_1$	Nodulating	T180, T202	Williams and Lynch, 1954 (as *no*);
$\underline{rj}_1$	Non-nodulating	T181, T201	symbol by Caldwell, 1966.
$\underline{Rj}_2$	Ineffective by strains b7, b14, and b122	Hardee	Caldwell, 1966.
$\underline{rj}_2$	Effective	c	
$\underline{Rj}_3$	Ineffective by strain 33	Hardee	Vest, 1970.
$\underline{rj}_3$	Effective	Clark	
$\underline{Rj}_4$	Ineffective by strain 61	Hill, Dunfield	Vest and Caldwell, 1972.
$\underline{rj}_4$	Effective	Lee, Semmes	

Table 1c. List of genes affecting growth and morphology of soybeans

Gene	Phenotype	Strain*	Reference
	1. Time of flowering & maturity		
$\underline{E}_1$	Late	T175	Owen, 1927b; Bernard, 1971.
$\underline{e}_1$	Early	Clark	
$\underline{E}_2$	Late	Clark	Bernard, 1971.
$\underline{e}_2$	Early	T245	
$\underline{E}_3$	Late and sensitive to fluorescent light	Harosoy 63	Buzzell, 1971; Kilen and Hartwig, 1971.
$\underline{e}_3$	Early and insensitive	Blackhawk	
	2. Stem		
$\underline{Dt}_1$	Indeterminate	Manchu, Clark	Woodworth, 1932, 1933; Bernard, 1972.
$\underline{dt}_1$	Determinate	Ebony, T245	
$\underline{Dt}_2$	Semi-determinate	T117	Bernard, 1972.
$\underline{dt}_2$	Indeterminate	Clark	
$\underline{F}$	Normal form	c	Nagai, 1926; Takagi, 1929; symbol by Woodworth, 1932, 1933; Matsura, 1933.
$\underline{f}$	Fasciated	T173	
	3. Inflorescence		
$\underline{Se}$	Pedunculate	T208	VanSchaik and Probst, 1958.
$\underline{se}$	Sub-sessile	T109	
	4. Leaf		
$\underline{Ab}$	Abscission at maturity	T161, c	Probst, 1950.
$\underline{ab}$	Delayed abscission	Kingwa	
$\underline{Lf}_1$	5-foliolate	T245	Takahaski and Fukuyama, 1919;
$\underline{lf}_1$	Trifoliolate	c	symbol by Fehr, 1972a.
$\underline{Lf}_2$	Trifoliolate	c	Fehr, 1972a.
$\underline{lf}_2$	7-foliolate	T255	
$\underline{Ln}$	Broad leaflet	c	Takahashi and Fukuyama, 1919.
$\underline{ln}$	Narrow, 4-seeded pods	T41	Woodworth, 1932, 1933; Takahashi, 1934; Domingo, 1945; symbol assigned here.
$\underline{Lo}$	Ovate	c	Domingo, 1945.
$\underline{lo}$	Oval, few-seeded pods	T122	

Table 1c. List of genes affecting growth and morphology of soybeans (continued)

Gene	Phenotype	Strain*	Reference
	5. Pubescence type		
A	Appressed	---	Karasawa, 1936; Ting, 1946; symbol by Morse and Cartter, 1937.
a	Erect	---	
P_1	Glabrous	T145	Nagai and Saito, 1923.
p_1	Pubescent	c	
P_2	Normal	c	Stewart and Wentz, 1926.
p_2	Puberulent	T31	
Pb	Sharp hair tip	PI 163.453, Kingwa	Ting, 1946.
pb	Blunt hair tip	Clark	
Pc	Normal	Clark	Bernard and Singh, 1969.
pc	Curly (deciduous)	T141	
Pd	Dense	T207	Bernard and Singh, 1969.
pd	Normal	Clark	
Ps	Sparse	T240	Bernard and Singh, 1969.
ps	Normal	Clark	
	6. Seed coat structure		
$B_1B_2B_3$	Bloom on seed coat	Sooty	Woodworth, 1932, 1933; Tang and Tai, 1962.
b_1, b_2, or b_3	No bloom	c	
N	Normal hilum abscission	c	Owen, 1928.
n	Lack of abscission layer	Soysota	

Table 1d. List of genes affecting nutrition, protein, or enzyme type, root fluorescence and glycosides

Gene	Phenotype	Strain*	Reference
	1. Reaction to nutritional factors		
Fe	Efficient iron utilization	c	Weiss, 1943.
fe	Inefficient	T203	
Np	Phosphorus tolerant	Chief	Bernard and Howell, 1964.
np	Sensitive to high P-level	Lincoln	
Ncl	Chloride excluding	Lee	Abel, 1969.
ncl	Chloride accumulating	Jackson	
	2. Seed protein or enzyme type		
—	A protein	Mandarin, Amsoy	Larsen and Caldwell, 1968, 1969.
—	B protein	Delmar, Kent	
Ep	High peroxidase activity	Harosoy 63	Buzzell and Buttery, 1969.
ep	Low peroxidase activity	Blackhawk	
Eu	Fast band urease	Blackhawk, Chippewa 64	Buttery and Buzzell, 1971.
eu	Slow band urease	Corsoy, Midwest	
Ti	Fast band trypsin inhibitor	Clark	Singh et al., 1969; Hymowitz and Hadley, 1972.
ti	Slow band trypsin inhibitor	T245	
	3. Root		
Fr	Fluorescent in u.v. light	Hawkeye, c	Fehr and Giese, 1971.
fr	Non-fluorescent	Minsoy	
	4. Kaempferol and quercetin glycosides of leaves		
Fg_1	Gentiobioside	T31, c	Buzzell, Buttery, and Haas, 1974.
fg_1	Monoglucoside	Chippewa 64, c	
Fg_2	Rutinoside	T31, c	Buzzell, Buttery, and Haas, 1974.
fg_2	Monoglucoside	Chippewa 64, c	
Fg_3	Sophoroside	T31, c	Buzzell, Buttery, and Haas, 1974.
fg_3	Monoglucoside	Chippewa 64, c	
Fg_4	Neohesperidoside	T31, c	Buzzell, Buttery, and Haas, 1974.
fg_4	Monoglucoside	AK (FC 30.761)	

Table 1e. List of genes causing sterility and dwarfness in soybeans

Gene	Phenotype	Strain*	Reference
$\frac{Df_2}{df_2}$	Normal "Lincoln" dwarf	Lincoln, c T243, T210	Porter and Weiss, 1948; symbol by Byth and Weber, 1969.
$\frac{Df_3}{df_3}$	Normal "Adams" dwarf	c T244	Byth and Weber, 1969.
$\frac{Df_4}{df_4}$	Normal Hark dwarf	c T256	Fehr, 1972b.
$\frac{Ms_1}{ms_1}$	Fertile Male-sterile	c N69-2819	Brim and Young, 1971.
$\frac{Pm}{pm}$	Normal Dwarf, crinkled leaves, sterile	c T211	Probst, 1950.
$\frac{St_2}{st_2}$	Fertile Asynaptic sterile	c T241	Hadley and Starnes, 1964.
$\frac{St_3}{st_3}$	Fertile Asynaptic sterile	c T242	Hadley and Starnes, 1964.
$\frac{St_4}{st_4}$	Fertile Desynaptic sterile	c T258	Palmer and Heer, 1974.

Table 1f. List of genes and cytoplasmic factors causing chlorophyll deficiency or retention in soybeans

Gene	Phenotype	Strain*	Reference
	1. Chlorophyll deficiency		
$\underline{V}_1$	Normal	c	Woodworth, 1932, 1933.
$\underline{v}_1$	Variegated	T93	
$\underline{Y}_3$	Normal	c	Nagai, 1926; Takagi, 1929, 1930; Terao and Nakatomi, 1929; symbol by Morse and Cartter, 1937.
$\underline{y}_3$	Turning yellow	Kura, T139	
$\underline{Y}_4$	Normal	c	Symbol by Morse and Cartter, 1937; Woodworth and Williams, 1938 (as $\underline{y}_5$ by error).
$\underline{y}_4$	Green-yellow, weak plant	T102	
$\underline{Y}_5$	Normal	c	Symbol by Morse and Cartter, 1937; Woodworth and Williams, 1938 (as $\underline{y}_4$ by error).
$\underline{y}_5$	Yellow-green, very weak plant	T116	
$\underline{Y}_6$	Normal	c	Symbol by Morse and Cartter, 1937; Woodworth and Williams, 1938.
$\underline{y}_6$	Pale green plant	T136	
$\underline{Y}_7$ or $\underline{Y}_8$	Normal	c	Morse and Cartter, 1937; Probst, 1950 (as $\underline{y}_8$); Williams, 1950.
$\underline{y}_7\underline{y}_8$	Yellow growth in cool weather	T138	
$\underline{Y}_9$	Normal	c	Probst, 1950.
$\underline{y}_9$	Bright greenish yellow	T135	
$\underline{Y}_{10}$	Normal	c	Probst, 1950.
$\underline{y}_{10}$	Yellow-green seedling, becoming green	T161	
$\underline{Y}_{11}$	Normal	c	Weber and Weiss, 1959.
$\underline{y}_{11}$	Lethal yellow	T219	
$\underline{Y}_{12}$	Normal	c	Weiss, 1970a.
$\underline{y}_{12}$	Whitish primary leaves	T233	

Table 1f. List of genes and cytoplasmic factors causing chlorophyll deficiency or retention in soybeans (continued)

Gene	Phenotype	Strain*	Reference
	1. Chlorophyll deficiency (cont'd)		
$\underline{Y}_{13}$	Normal	c	Weiss, 1970e.
$\underline{y}_{13}$	Whitish green seedling	T230	
$\underline{Y}_{16}$	Normal	c	Wilcox and Probst, 1969.
$\underline{y}_{16}$	Nearly white lethal	T257	
$\underline{Y}_{18}$	Normal	c	Peterson and Weber, 1969.
$\underline{Y}^{M}_{18}$	Unstable	T225	
$\underline{y}_{18}$	Near lethal yellow	T225	
	2. Chlorophyll retention		
cyt-Y	Yellow seed embryo	c	Terao, 1918; Veatch and Woodworth, 1930.
cyt-G	Green seed embryo	T104, Medium Green	
$\underline{D}_1$ or $\underline{D}_2$	Yellow seed embryo	c	Woodworth, 1921; Owen, 1927a; Veatch and Woodworth, 1930.
$\underline{d}_1\underline{d}_2$	Green seed embryo	Columbia	
G	Green seed coat	Kura	Terao, 1918; Takahashi and Fukuyama, 1919; Nagai, 1921; Woodworth, 1921.
g	Yellow seed coat	c	

Table 1g. List of genes affecting pigmentation in soybeans

Gene	Phenotype	Strain*	Reference
I	Light hilum	Mandarin	Nagai, 1921; Nagai and Saito, 1923; Owen, 1928; Woodworth, 1932, 1933; Mahmud and Probst, 1953.
i^i	Dark hilum	Manchu	
i^k	Saddle pattern	Black Eyebrow	
i	Self dark seed	Soysota	
Im	Non-mottling seed	Merit	Cooper, 1966.
im	Dark mottling on seed	Harosoy	
K	Black or brown hilum	c	Takagi, 1929, 1930; Williams, 1958.
k	Black or brown saddle	Kura, T153	
L_1L_2	Black pod	Seneca	Bernard, 1967.
L_1l_2	Black pod	T215	
l_1L_2	Brown pod	Clark	
l_1l_2	Tan pod	Dunfield	
O	Brown seed	Soysota	Nagai, 1921; Weiss, 1970b.
o	Reddish brown seed	Ogema	
R	Black seed	c	Nagai, 1921; Woodworth, 1921; Stewart, 1930; Williams, 1952.
r	Brown seed	c	
r^m	Black stripes on brown seed	T125	Nagai and Saito, 1923; Weiss, 1970b.
T	Tawny (brown) pubescence	c	Piper and Morse, 1910; Nagai, 1921 (as C c); Woodworth, 1921; Williams, 1952.
t	Gray pubescence	c	
W_1	Purple flower	c	Takahashi and Fukuyama, 1919; Woodworth, 1923.
w_1	White flower	c	
W_3W_4	Dilute purple flower	Laredo	Hartwig and Hinson, 1962.
w_3W_4	Purple flower	c	
W_3w_4	Dark purple flower	—	
w_3w_4	Near white flower	—	
Wm	Purple flower	c	Buzzell, Bernard, and Buttery, 1974.
wm	Magenta flower	T235	

* c indicates that the gene commonly occurs in many varieties.

Table 2. Notice of release of isolines of Clark and Harosoy soybeans

The Illinois Agriculture Experiment Station and the Plant Science Research Division, Agricultural Research Service, announce the release of the near-isogenic lines of soybeans described on the attached list. The lines are categorized by differences from the recurrent parent in (1) chlorophyll, (2) stem growth, (3) time of maturity, (4) leaf form, (5) pubescence type, (6) disease reaction, (7) nutrient response, and (8) pigmentation.

These lines were developed at the U.S. Regional Soybean Laboratory from the adapted commercial varieties Clark (maturity group IV) and Harosoy (maturity group II), and originated as plant selections from the indicated backcrosses (usually BC_5), backcross combinations, or mutants. They are homozygous for the genes described (except for lethal $\underline{y}_{11}$) and have been selected for similarity to the recurrent parent for other traits. They involve 38 different nuclear genes and the cytoplasmic factor cyt-G, which may be useful in genetic and other research. Some have a demonstrated or potential use in commercial variety development. The attached list only briefly describes the gene effects, and reference should be made to pertinent technical literature for more details. A list of references to gene symbols and a description of the T strains are available in a report (RSLM 245) on the Soybean Genetic Type Collection issued by the U.S. Regional Soybean Laboratory.

A seed packet (30 seeds) of each line will be made available for research purposes only, upon request to R. L. Bernard, U.S. Regional Soybean Laboratory, Urbana, Ill. 61801.

Isolines of Clark and Harosoy Soybeans

The following is a list of soybean lines nearly isogenic to the varieties Clark and Harosoy. The Descriptive Designation is made up of the recurrent variety name plus the symbol of the transferred gene or cytoplasmic factor. The Line Designation identifies the specific homozygous line available, usually an F_2 or F_3 plant progeny. In some instances, two or more lines are listed if the most nearly isogenic one has not yet been

identified. In the parentage column, Clark is abbreviated C, and Harosoy is H. Disease resistant isolines, L6 (Clark-Rps rxp) and L2 (Harosoy-Rps rxp), were used in some cases as the recurrent parent. The superscript is the number of times the recurrent parent was crossed to. In some cases alternate BC_5 lines from other donor parents [indicated in brackets] are available.

Descriptive Designation	Line Designation	Parentage & [alternate donor]
	1. Chlorophyll	
	Clark = Harosoy - cyt-Y g D_1 D_2 Y_3 Y_7 Y_8 Y_9 Y_{11}	
Green seed (maternally inherited)		
Clark — cyt-G	L62-1027	Medium Green x C_7^7
Harosoy — cyt-G	L62-17	Medium Green x H^7
Green seed		
Clark — G d_1d_2	L64-2545, L67-984	C_6^6 x Columbia
Clark — d_1d_2	L69-4663, L69-4664	C_6^6 x Columbia
Harosoy — $G^2d_1d_2$	L64-2489	H^6 x Columbia
Harosoy — d_1d_2	L69-4267	H^6 x Columbia
Green seed coat		
Clark — G d_1	L69-4659, L69-4660	C_6^6 x Columbia
Clark — G d_2	L69-4666	C_6^6 x Columbia
Harosoy — G^2d_1	L69-4265	H^6 x Columbia
Harosoy — G d_2	L67-971	H^6 x Columbia
Yellow seed (indistinguishable from recurrent parent)		
Clark — d_2	L69-4662	C_6^6 x Columbia
Harosoy — d_2	L69-4266	H^6 x Columbia
Plant turning yellow		
Clark — y_3	L63-2346B	C^6 x T139
Clark — y_3 cyt-G	L64-2584	L62-1027 (cyt-G) x L63-2345 (y_3)
Harosoy — y_3	L63-1016	H^6 x T139
Yellow growth when cool		
Clark — y_7y_8	L63-1792	C_6^6 x T138
Harosoy — y_7y_8	L68-560	H^6 x T138
Bright yellow-green leaves		
Clark — y_9 †	L69-4755, L69-4756	$L6_6^6$ x T135
Harosoy — y_9 †	L69-4318	$L2^6$ x T135
Lethal, semi-dominant yellow plant		
Clark — $Y_{11}y_{11}$	L72-1937, L72-1939	C^5 x (C-k x T219)

Descriptive Designation	Line Designation	Parentage & [alternate donor]
2. Stem Growth		
Clark = Harosoy = $\underline{Dt_1}$ $\underline{dt_2}$ $\underline{F}$		
Determinate stem		
Clark – $\underline{dt_1}$	L63-3297	C^6 x T141 [T217,T245, T248,PI 84946-2]
Harosoy – $\underline{dt_1}$	L62-973	H^6 x T245 [Higan, T145,T204]
Semi-determinate		
Clark – $\underline{Dt_2}$	L62-1251	C^6 x T117
Harosoy – $\underline{Dt_2}$*	L62-361, L62-364	H^6 x T117 [T207]
Fasciated		
Clark – $\underline{f}$	L65-763	C^6 x T248
Harosoy – $\underline{f}$	L65-756	H^6 x T248
Combination		
Harosoy – $\underline{dt_1}$ $\underline{Dt_2}$	L67-3256	(H^6 x T117) ($\underline{Dt_2}$) x L62-973 ($\underline{dt_1}$)
3. Time of Maturity		
Clark = $\underline{e_1}$ $\underline{T}$ $\underline{E_2}$, Harosoy = $\underline{e_1}$ $\underline{t}$		
Late		
Clark – $\underline{E_1}$	L67-1474	C^6 x T175 [T204]
Clark – $\underline{E_1}$ $\underline{t}$	L65-3366, L65-3396	C^6 x T175 [T204]
Harosoy – $\underline{E_1}$	L68-694	H^6 x T217 [Columbia, T175]
Harosoy – $\underline{E_1}$ $\underline{T}$	L67-2324	H^6 x T217 [Columbia, T175]
Early		
Clark – $\underline{e_2}$	L62-1932, L63-3117	C^6 x T245 [T203,T207, T217, PI 84946-2]
Combination		
Clark – $\underline{E_1}$ $\underline{t}$ $\underline{e_2}$	L66-432	L62-1932 ($\underline{e_2}$) x L65-3366 ($\underline{E_1}$ $\underline{t}$)
Combinations of stem and maturity genes		
Clark – $\underline{dt_1}$ $\underline{E_1}$ $\underline{t}$	L66-546	(C^6 x T245) ($\underline{dt_1}$ $\underline{e_2}$) x L65-3366 ($\underline{E_1}$ $\underline{t}$)
Clark – $\underline{dt_1}$ $\underline{E_1}$ $\underline{t}$ $\underline{e_2}$	L66-531	(C^6 x T245) ($\underline{dt_1}$ $\underline{e_2}$) x L65-3366 ($\underline{E_1}$ $\underline{t}$)
Clark – $\underline{dt_1}$ $\underline{e_2}$	L65-778	C^6 x T245
Clark – $\underline{dt_1}$ $\underline{e_2}$	L67-3218	L62-1932 ($\underline{e_2}$) x L63-3297 ($\underline{dt_1}$)
Clark – $\underline{Dt_2}$ $\underline{e_2}$	L67-3232	L62-1932 ($\underline{e_2}$) x L62-1251 ($\underline{Dt_2}$)

Descriptive Designation	Line Designation	Parentage & [alternate donor]
4. Leaf Form		
Clark = Harosoy = $\underline{lf_1}$ $\underline{Ln}$ $\underline{Lo}$		
Five leaflet		
Clark — $\underline{Lf_1}$	L64-1344	C^6 x T245
Harosoy — $\underline{Lf_1}$	L62-956	H^6 x T245
Narrow leaflet		
Clark — $\underline{ln}$*	L62-1579	C^6 x T204
Harosoy — $\underline{ln}$	L63-1212	H^6 x T204
Oval leaflet		
Clark — $\underline{lo}$*	L62-1615	C^6 x T204
Harosoy — $\underline{lo}$	L65-372	H^6 x T204
Combinations		
Clark — $\underline{Lf_1}$ $\underline{ln}$, $\underline{ln}$ $\underline{lo}$, $\underline{Lf_1}$ $\underline{Dt_2}$, $\underline{ln}$ $\underline{Dt_2}$, $\underline{Lf_1}$ $\underline{ln}$ $\underline{Dt_2}$, $\underline{Lf_1}$ $\underline{dt_1}$, $\underline{Lf_1}$ $\underline{e_2}$		
Harosoy — $\underline{Lf_1}$ $\underline{ln}$, $\underline{ln}$ $\underline{lo}$, $\underline{Lf_1}$ $\underline{Dt_2}$, $\underline{ln}$ $\underline{Dt_2}$, $\underline{Lf_1}$ $\underline{ln}$ $\underline{Dt_2}$		
5. Pubescence Type		
Clark = Harosoy = $\underline{p_1}$ $\underline{P_2}$ $\underline{Pc}$ $\underline{pd}$ $\underline{ps}$		
Glabrous		
Clark — $\underline{P_1}$	L62-1385	C^6 x T145
Harosoy — $\underline{P_1}$	L62-561	H^6 x T145
Puberulent		
Clark — $\underline{p_2}$ $\underline{I}$ $\underline{r}$ †	L70-4049	L6-I r^6 x T31
Harosoy — $\underline{p_2}$ †	L70-4001	$L2^6$ x T31
Curly		
Clark — $\underline{pc}$	L63-2435	C^6 x T141
Harosoy — $\underline{pc}$	L63-1097	H^6 x T141
Dense		
Clark — $\underline{Pd}$	L62-1686	C^6 x T207
Harosoy — $\underline{Pd}$*	L62-801	H^6 x T207
Sparse		
Clark — $\underline{Ps}$	L63-2999	C^6 x T240
Harosoy — $\underline{Ps}$	L62-880	H^6 x T240
Combinations		
Clark — $\underline{P_1pc}$, $\underline{P_1Pd}$, $\underline{P_1Ps}$, $\underline{pc}$ $\underline{Pd}$, $\underline{pc}$ $\underline{Ps}$, $\underline{Pd}$ $\underline{Ps}$, $\underline{P_1}$ $\underline{r}$		
Harosoy — $\underline{P_1pc}$, $\underline{P_1Pd}$, $\underline{P_1Ps}$, $\underline{pc}$ $\underline{Pd}$, $\underline{pc}$ $\underline{Ps}$, $\underline{Pd}$ $\underline{Ps}$		

Descriptive Designation	Line Designation	Parentage & [alternate donor]
	6. Disease Reaction	
	Clark = Harosoy = rpm rps Rxp	
Phytophthora root rot resistance		
Clark — Rps	L61-4222 (L7 line)	C^8 x Blackhawk
Harosoy — Rps	L59-731 (Harosoy 63 line)	H^8 x Blackhawk
Bacterial pustule resistant		
Clark — rxp	L61-4180 (L8 line)	C^8 x CNS
Harosoy — rxp	L61-4096 (L3 line)	H^6 x S54-1207 (rxp from CNS)
Combinations		
Clark — Rps rxp	L60-246 (Clark 63 line)	(C^7 x CNS) x (C^6 x Blackhawk)
Clark — Rps rxp	L61-5448 (L6 line)	(C^8 x CNS) x (C^8 x Blackhawk)
Harosoy — Rps rxp	L61-5047 (L2 line)	(H^8 x Blackhawk) x (H^6 x S54-1207)
Harosoy — Rps rxp	L68-758	H^4 x L2
	7. Nutrient Response	
	Clark = Harosoy = Fe np Rj_1	
Iron inefficient		
Clark — fe	L65-1255, L65-1257	C^6 x T203
Harosoy — fe	L66-731, L66-781	H^6 x T203
Phosphorus tolerant		
Clark — Np*	L63-1677	C^6 x Chief
Harosoy — Np	L66-704	H^6 x Clark — Np
Non-nodulating		
Clark — rj_1	L63-1889	C^6 x T201
Harosoy — rj_1	L65-1274	H^6 x T201

Descriptive Designation	Line Designation	Parentage & [alternate donor]
8. Pigmentation		
Clark = $\underline{i}^{i}$ $\underline{R}$ $\underline{T}$ (black hilum), Harosoy = $\underline{I}$ $\underline{r}$ $\underline{t}$ (yellow hilum)		
Clark = Harosoy = $\underline{W}_1$ $\underline{im}$ $\underline{b}_1$ $\underline{l}_1$ $\underline{L}_2$		
Gray (Clark — $\underline{I}$) or buff (Harosoy — $\underline{i}^{i}$) hilum		
Clark — $\underline{I}$	L62-1058	C^6 x T201
Harosoy — $\underline{i}^{i}$	L67-38	H^6 x Clark [Columbia, T117,T176]
Self black (Clark — $\underline{i}$) or buff (Harosoy — $\underline{i}$) seed		
Clark — $\underline{i}$*	L67-3469	C mutation [T106-2]
Harosoy — $\underline{i}$*	L67-3388	H mutation
Black saddle on seed		
Clark — $\underline{i}^{k}$ †	L70-4204, L70-4209	C63-$\underline{i}^6$ x Black Eyebrow
Clark — $\underline{k}$*	L67-3479	C mutation
Brown (Clark — $\underline{r}$) or gray (Harosoy — $\underline{R}$) hilum		
Clark — $\underline{r}$*	L62-1383	C^6 x T145 [Higan, PI 84946-2]
Harosoy — $\underline{R}$	L65-540	H^6 x T176 [T139]
Gray (Clark — $\underline{t}$) or tawny (Harosoy — $\underline{T}$) pubescence		
Clark — $\underline{t}$	L67-483, L68-1029	C^6 x Higan [T176]
Harosoy — $\underline{T}$	L66-707	H^6 x Clark
White flower		
Clark — $\underline{w}_1$*	L63-2373	C^6 x T139 [Seneca, T204,T248]
Harosoy — $\underline{w}_1$	L62-906	H^6 x T240
Non-mottling, self yellow seed		
Clark — $\underline{Im}$ $\underline{I}$ $\underline{r}$ †	L69-5338	L6-$\underline{I}$ $\underline{r}^6$ x Hawkeye
Clark — $\underline{Im}$ $\underline{r}$ †	L69-5366	L6-$\underline{I}$ $\underline{r}^6$ x Hawkeye
Bloom on black seed		
Clark — $\underline{B}_1$ $\underline{i}$	L69-4544, L68-1149	C — $\underline{i}^6$ x Sooty
Black pod		
Clark — $\underline{L}_1$ †	L68-1562	$L6^6$ x Seneca [T247, Laredo]
Harosoy — $\underline{L}_1$ †	L68-582	$L2^6$ x Seneca [T247]
Tan pod		
Clark — $\underline{l}_2$	L68-1013	C^6 x Higan [T204]
Harosoy — $\underline{l}_2$	L67-226	H^6 x Higan [T145]

Descriptive Designation	Line Designation	Parentage & [alternate donor]
	8. Pigmentation (cont'd)	
Combinations		
Clark –	I r*, I r t †, I r t w_1 †; i r*, i t, i w_1, i t w_1; r w_1 †; t w_1, r t w_1 †; k I, k r, k I r, k t, k w_1, k t w_1; l_2 w_1, l_2 t, ln t	
Harosoy –	Dt_2 i^i, i^i Np, l_2P_1, Np I, ln t, R i^i	

†Only available in combination with Rps rxp (phytophthora and pustule resistance.)

*Also available in combination with Rps rxp (phytophthora and pustule resistance.)

†Table 3. Genetic linkage groups in the soybean

Linkage Group	Linkage Intensity Map	Linked Genes	
1	$\underline{y}_{12}$ ←20.2±1.1%→ $\underline{E}_1$ ←3.9±.4%→ $\underline{t}$ ←21.6±.7%→	$\underline{E}_1$ $\underline{t}$ $\underline{y}_{12}$	late maturity gray pubescence chlorophyll deficient
2	$\underline{P}_1$ ←20.9±2.4%→ $\underline{r}$	$\underline{P}_1$ $\underline{r}$	glabrous brown seed
3	$\underline{G}$ ←4.2±.6%→ $\underline{d}_1$	$\underline{G}$ $\underline{d}_1$	green seed coat green seed embryo
4	$\underline{v}_1$ ←35.6±.9%→ $\underline{ln}$* ←26.4±1.4%→ $\underline{p}_2$ ←independent→	$\underline{ln}$ $\underline{p}_2$ $\underline{v}_1$	narrow leaf puberulent plant variegated leaf
5	$\underline{dt}_1$ ←39.4±1.8%→ $\underline{L}_1$	$\underline{dt}_1$ $\underline{L}_1$	determinate stem black pod
6	$\underline{df}_2$ ←12.1±.7%→ $\underline{y}_{11}$	$\underline{df}_2$ $\underline{y}_{11}$	"Lincoln" dwarf chlorophyll deficient
7	$\underline{y}_{13}$ ←31.3±1.9%→ $\underline{o}$ ←17.8±.7%→ $\underline{i}$ ←41.1±.9%→	$\underline{i}$ $\underline{o}$ $\underline{y}_{13}$	self dark seed coat red brown seed coat chlorophyll deficient

*Formerly na.

For preliminary information on additional linkages, see:

$\underline{Fg}_3 - \underline{Fg}_4$ Buzzell, 1974. SGN 1:11-14.

$\underline{fg}_4 - \underline{T}_1$ Buzzell, 1974. SGN 1:11-14.

$\underline{W}_1 - \underline{wm}$ Buzzell, Bernard, and Buttery, 1974. SGN 1:14-15.

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†Table 3 is taken from ASA Monograph No. 16, Chapter 4, "Qualitative Genetics," by R. L. Bernard and M. G. Weiss, and cannot be copied without specific permission from the American Society of Agronomy.

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VII. GENETIC STOCKS DESIRED

1) Tadao Nagata
Faculty of Agriculture
Kobe University
Rokkodai, Kobe 657, Japan

1. Cytoplasmic male sterile strains
2. Drought resistant strains
3. Highest lodging resistant strains
4. Semi-wild strains similar to Glycine gracilis found in other regions than Northeast district of China

2) James A. Lackey
Botany Department
Iowa State University
Ames, Iowa 50010

1. Any available species from the following genera:

Dioclea H.B.&K.
Dumasia DC.
Endomallus Gagep.
Neorautaenenia Schinz
Ophrestia H.M.L. Forges (Paraglycine F.J. Hermann, and Pseudoglycine F.J. Hermann) I do not need any more O. radicosa or O. hedysaroides.
Platycyamus Benth.
Shuteria Wight & Arn.

2. The following species:

Amphicarpaea africana (Hook.f.) Harms
Clitoriopsis mollis Wilczek
Diphyllarium mekongense Gagnep.
Glycine latrobeana (Meissm.) Benth.
Herpyza grandiflora (Griseb.) Ch. Wright
Teyleria koordersii (Backer) Backer
Vandasia retusa (Benth.) Domin.

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